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(54) Title: FUSION PROTEINS OF <i>MYCOBACTERIUM TUBERCULOSIS</i> ANTIGENS AND THEIR USES			
(57) Abstract <p>The present invention relates to fusion proteins containing at least two <i>Mycobacterium tuberculosis</i> antigens. In particular, it relates to bi-fusion proteins which contain two individual <i>M. tuberculosis</i> antigens, tri-fusion proteins which contain three <i>M. tuberculosis</i> antigens, tetra-fusion proteins which contain four <i>M. tuberculosis</i> antigens, and penta-fusion proteins which contain five <i>M. tuberculosis</i> antigens, and methods for their use in the diagnosis, treatment and prevention of tuberculosis infection.</p>			

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FUSION PROTEINS OF *MYCOBACTERIUM* *TUBERCULOSIS* ANTIGENS AND THEIR USES

5 1. INTRODUCTION

The present invention relates to fusion proteins containing at least two *Mycobacterium tuberculosis* antigens. In particular, it relates to bi- fusion proteins which contain two individual *M. tuberculosis* antigens, tri- fusion proteins which contain three *M.*
10 *tuberculosis* antigens, tetra-fusion proteins which contain four *M. tuberculosis* antigens, and penta-fusion proteins which contain five *M. tuberculosis* antigens, and methods for their use in the diagnosis, treatment and prevention of tuberculosis infection.

15 2. BACKGROUND OF THE INVENTION

Tuberculosis is a chronic infectious disease caused by infection with *M. tuberculosis*. It is a major disease in developing countries, as well as an increasing problem in developed areas of the world, with about 8 million new cases and 3 million deaths each year. Although the infection may be asymptomatic for a considerable period of time, the
20 disease is most commonly manifested as an acute inflammation of the lungs, resulting in fever and a nonproductive cough. If untreated, serious complications and death typically result.

Although tuberculosis can generally be controlled using extended antibiotic therapy, such treatment is not sufficient to prevent the spread of the disease. Infected individuals
25 may be asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behavior is difficult to monitor. Some patients do not complete the course of treatment, which can lead to ineffective treatment and the development of drug resistance.

In order to control the spread of tuberculosis, effective vaccination and accurate
30 early diagnosis of the disease are of utmost importance. Currently, vaccination with live bacteria is the most efficient method for inducing protective immunity. The most common *Mycobacterium* employed for this purpose is *Bacillus Calmette-Guerin* (BCG), an avirulent strain of *M. bovis*. However, the safety and efficacy of BCG is a source of controversy and some countries, such as the United States, do not vaccinate the general public with this
35 agent.

Diagnosis of tuberculosis is commonly achieved using a skin test, which involves intradermal exposure to tuberculin PPD (protein-purified derivative). Antigen-specific T cell responses result in measurable induration at the injection site by 48-72 hours after injection, which indicates exposure to Mycobacterial antigens. Sensitivity and specificity
5 have, however, been a problem with this test, and individuals vaccinated with BCG cannot be distinguished from infected individuals.

While macrophages have been shown to act as the principal effectors of *M. tuberculosis* immunity, T cells are the predominant inducers of such immunity. The essential role of T cells in protection against *M. tuberculosis* infection is illustrated by the
10 frequent occurrence of *M. tuberculosis* in Acquired Immunodeficiency Syndrome patients, due to the depletion of CD4⁺ T cells associated with human immunodeficiency virus (HIV) infection. Mycobacterium-reactive CD4⁺ T cells have been shown to be potent producers of gamma-interferon (IFN- γ), which, in turn, has been shown to trigger the anti-mycobacterial effects of macrophages in mice. While the role of IFN- γ in humans is less clear, studies
15 have shown that 1,25-dihydroxy-vitamin D3, either alone or in combination with IFN- γ or tumor necrosis factor-alpha, activates human macrophages to inhibit *M. tuberculosis* infection. Furthermore, it is known that IFN- γ stimulates human macrophages to make 1,25-dihydroxy-vitamin D3. Similarly, interleukin-12 (IL-12) has been shown to play a role in stimulating resistance to *M. tuberculosis* infection. For a review of the immunology of
20 *M. tuberculosis* infection, see Chan and Kaufmann, 1994, *Tuberculosis: Pathogenesis, Protection and Control*, Bloom (ed.), ASM Press, Washington, DC.

Accordingly, there is a need for improved vaccines, and improved methods for diagnosis, preventing and treating tuberculosis.

25 3. SUMMARY OF THE INVENTION

The present invention relates to fusion proteins of *M. tuberculosis* antigens. In particular, it relates to fusion polypeptides that contain two or more *M. tuberculosis* antigens, polynucleotides encoding such polypeptides, methods of using the polypeptides
30 and polynucleotides in the diagnosis, treatment and prevention of *M. tuberculosis* infection.

The present invention is based, in part, on the inventors' discovery that polynucleotides which contain two to five *M. tuberculosis* coding sequences produce recombinant fusion proteins that retain the immunogenicity and antigenicity of their individual components. The fusion proteins described herein induced both T cell and B cell
35 responses, as measured by T cell proliferation, cytokine production, and antibody

production. Furthermore, a fusion protein was used as an immunogen with adjuvants *in vivo* to elicit both cell-mediated and humoral immunity to *M. tuberculosis*. Additionally, a fusion protein was made by a fusion construct and used in a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis.

- 5 The fusion protein was a more effective immunogen than a mixture of its individual protein components.

In a specific embodiment of the invention, the isolated or purified *M. tuberculosis* polypeptides of the invention may be formulated as pharmaceutical compositions for administration into a subject in the prevention and/or treatment of *M. tuberculosis* infection.

- 10 The immunogenicity of the fusion protein may be enhanced by the inclusion of an adjuvant.

In another aspect of the invention, the isolated or purified polynucleotides are used to produce recombinant fusion polypeptide antigens *in vitro*. Alternatively, the polynucleotides may be administered directly into a subject as DNA vaccines to cause
15 antigen expression in the subject, and the subsequent induction of an anti-*M. tuberculosis* immune response.

- It is also an object of the invention that the polypeptides be used in *in vitro* assays for detecting humoral antibodies or cell-mediated immunity against *M. tuberculosis* for diagnosis of infection or monitor of disease progression. Additionally, the polypeptides
20 may be used as an *in vivo* diagnostic agent in the form of an intradermal skin test. Alternatively, the polypeptides may be used as immunogens to generate anti-*M. tuberculosis* antibodies in a non-human animal. The antibodies can be used to detect the target antigens *in vivo* and *in vitro*.

25

4. BRIEF DESCRIPTION OF THE DRAWINGS

- Figure 1A and 1B. The nucleotide sequence (SEQ ID NO:1) and amino acid
30 sequence (SEQ ID NO:2) of tri-fusion protein Ra12-TbH9-Ra35 (designated Mtb32A).
- Figure 2 : The nucleotide sequence (SEQ ID NO:3) and amino acid
sequence (SEQ ID NO:4) of tri-fusion protein Erd14-DPV-MTI (designated Mtb39A).
- Figure 3A - 3D: The nucleotide sequence (SEQ ID NO:5) and amino acid
35 sequence (SEQ ID NO:6) of tri-fusion protein TbRa3-38kD-

- 5
- Figure 4A - 4D: Tb38-1. The nucleotide sequence (SEQ ID NO:7) and amino acid sequence (SEQ ID NO:8) of bi-fusion protein TbH9-Tb38-1.
- Figure 5A - 5J: The nucleotide sequence (SEQ ID NO:9) and amino acid sequence (SEQ ID NO:10) of tetra-fusion protein TbRa3-38kD-Tb38-1-DPEP (designated TbF-2).
- Figure 6A and 6B: The nucleotide sequence (SEQ ID NO:11) and amino acid sequence (SEQ ID NO:12) of penta-fusion protein Erd14-DPV-MTI-MSL-MTCC2 (designated Mtb88f).
- 10 Figure 7A and 7B: The nucleotide sequence (SEQ ID NO:13) and amino acid sequence (SEQ ID NO:14) of tetra-fusion protein Erd14-DPV-MTI-MSL (designated Mtb46f).
- Figure 8A and 8B: The nucleotide sequence (SEQ ID NO:15) and amino acid sequence (SEQ ID NO:16) of tetra-fusion protein DPV-MTI-MSL-MTCC2 (designated Mtb71f).
- 15 Figure 9A and 9B: The nucleotide sequence (SEQ ID NO:17) and amino acid sequence (SEQ ID NO:18) of tri-fusion protein DPV-MTI-MSL (designated Mtb31f).
- Figure 10A and 10B: The nucleotide sequence (SEQ ID NO:19) and amino acid sequence (SEQ ID NO:20) of tri-fusion protein TbH9-DPV-MTI (designated Mtb61f).
- 20 Figure 11A and 11B: The nucleotide sequence (SEQ ID NO:21) and amino acid sequence (SEQ ID NO:22) of tri-fusion protein Erd14-DPV-MTI (designated Mtb36f).
- 25 Figure 12A and 12B: The nucleotide sequence (SEQ ID NO:23) and amino acid sequence (SEQ ID NO:24) of bi-fusion protein TbH9-Ra35 (designated Mtb59f).
- Figure 13A and 13B: The nucleotide sequence (SEQ ID NO:25) and amino acid sequence (SEQ ID NO:26) of bi-fusion protein Ra12-DPPD (designated Mtb24).
- 30 Figure 14A-14F: T cell proliferation responses of six PPD+ subjects when stimulated with two fusion proteins and their individual components.
- 35 Figure 15A-15F: IFN- γ production of six PPD+ subjects when stimulated with two fusion proteins and their individual components.

- Figure 16A-16F: T cell proliferation of mice immunized with a fusion protein or its individual components and an adjuvant.
- Figure 17: IFN- γ production of mice immunized with a fusion protein or its individual components and an adjuvant.
- 5 Figure 18: IL-4 production of mice immunized with a fusion protein or its individual components and an adjuvant.
- Figure 19A-19F: Serum antibody concentrations of mice immunized with a fusion protein or its individual components and an adjuvant.
- 10 Figure 20A-20C: Survival of guinea pigs after aerosol challenge of *M. tuberculosis*. Fusion proteins, Mtb32A and Mtb39A, were formulated in adjuvant SBAS1c (20A), SBAS2 (20B) or SBAS7 (20C), and used as an immunogen in guinea pigs prior to challenge with bacteria. BCG is the positive control.
- 15 Figure 21A and 21B: Stimulation of proliferation and IFN- γ production in TbH9-specific T cells by the fusion protein TbH9-Tb38-1.
- Figure 22A and 22B: Stimulation of proliferation and IFN- γ production in Tb38-1-specific T cells by the fusion protein TbH9-Tb38-1.
- 20 Figure 23A and 23B: Stimulation of proliferation and IFN- γ production in T cells previously shown to respond to both TbH-9 and Tb38-1 antigens by the fusion protein TbH9-Tb38-1.

5. DETAILED DESCRIPTION OF THE INVENTION

25 The present invention relates to antigens useful for the treatment and prevention of tuberculosis, polynucleotides encoding such antigens, and methods for their use. The antigens of the present invention are fusion polypeptides of *M. tuberculosis* antigens and variants thereof. More specifically, the antigens of the present invention comprise at least two polypeptides of *M. tuberculosis* that are fused into a larger fusion polypeptide molecule. The antigens of the present invention may further comprise other components
30 designed to enhance the immunogenicity of the antigens or to improve these antigens in other aspects, for example, the isolation of these antigens through addition of a stretch of histidine residues at one end of the antigen.

5.1. M. TUBERCULOSIS SPECIFIC ANTIGENS

35 The antigens of the present invention are exemplified in Figures 1A through 13B,

including homologues and variants of those antigens. These antigens may be modified, for example, by adding linker peptide sequences as described below. These linker peptides may be inserted between one or more polypeptides which make up each of the fusion proteins presented in Figures 1A through 13B. Other antigens of the present invention are
5 antigens described in Figures 1A through 13B which have been linked to a known antigen of *M. tuberculosis*, such as the previously described 38 kD (SEQ ID NO:27) antigen (Andersen and Hansen, 1989, Infect. Immun. 57:2481-2488; Genbank Accession No. M30046).

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5.2. IMMUNOGENICITY ASSAYS

Antigens described herein, and immunogenic portions thereof, have the ability to induce an immunogenic response. More specifically, the antigens have the ability to induce proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production)
15 in T cells, NK cells, B cells and/or macrophages derived from an *M. tuberculosis*-immune individual. The selection of cell type for use in evaluating an immunogenic response to a antigen will depend on the desired response. For example, interleukin-12 production is most readily evaluated using preparations containing B cells and/or macrophages. An *M. tuberculosis*-immune individual is one who is considered to be resistant to the
20 development of tuberculosis by virtue of having mounted an effective T cell response to *M. tuberculosis* (*i.e.*, substantially free of disease symptoms). Such individuals may be identified based on a strongly positive (*i.e.*, greater than about 10 mm diameter induration) intradermal skin test response to tuberculosis proteins (PPD) and an absence of any signs or symptoms of tuberculosis disease. T cells, NK cells, B cells and macrophages derived from
25 *M. tuberculosis*-immune individuals may be prepared using methods known to those of ordinary skill in the art. For example, a preparation of PBMCs (*i.e.*, peripheral blood mononuclear cells) may be employed without further separation of component cells. PBMCs may generally be prepared, for example, using density centrifugation through "FICOLL" (Winthrop Laboratories, NY). T cells for use in the assays described herein may
30 also be purified directly from PBMCs. Alternatively, an enriched T cell line reactive against mycobacterial proteins, or T cell clones reactive to individual mycobacterial proteins, may be employed. Such T cell clones may be generated by, for example, culturing PBMCs from *M. tuberculosis*-immune individuals with mycobacterial proteins for a period of 2-4 weeks. This allows expansion of only the mycobacterial protein-specific T cells,
35 resulting in a line composed solely of such cells. These cells may then be cloned and tested

with individual proteins, using methods known to those of ordinary skill in the art, to more accurately define individual T cell specificity. In general, antigens that test positive in assays for proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) performed using T cells, NK cells, B cells and/or macrophages derived from an
5 *M. tuberculosis*-immune individual are considered immunogenic. Such assays may be performed, for example, using the representative procedures described below. Immunogenic portions of such antigens may be identified using similar assays, and may be present within the polypeptides described herein.

The ability of a polypeptide (*e.g.*, an immunogenic antigen, or a portion or other
10 variant thereof) to induce cell proliferation is evaluated by contacting the cells (*e.g.*, T cells and/or NK cells) with the polypeptide and measuring the proliferation of the cells. In general, the amount of polypeptide that is sufficient for evaluation of about 10^5 cells ranges from about 10 ng/mL to about 100 μ g/mL and preferably is about 10 μ g/mL. The incubation of polypeptide with cells is typically performed at 37°C for about six days.
15 Following incubation with polypeptide, the cells are assayed for a proliferative response, which may be evaluated by methods known to those of ordinary skill in the art, such as exposing cells to a pulse of radiolabeled thymidine and measuring the incorporation of label into cellular DNA. In general, a polypeptide that results in at least a three fold increase in proliferation above background (*i.e.*, the proliferation observed for cells cultured without
20 polypeptide) is considered to be able to induce proliferation.

The ability of a polypeptide to stimulate the production of interferon- γ and/or interleukin-12 in cells may be evaluated by contacting the cells with the polypeptide and measuring the level of interferon- γ or interleukin-12 produced by the cells. In general, the amount of polypeptide that is sufficient for the evaluation of about 10^5 cells ranges from
25 about 10 ng/mL to about 100 μ g/mL and preferably is about 10 μ g/mL. The polypeptide may be, but need not be, immobilized on a solid support, such as a bead or a biodegradable microsphere, such as those described in U.S. Patent Nos. 4,897,268 and 5,075,109. The incubation of polypeptide with the cells is typically performed at 37°C for about six days. Following incubation with polypeptide, the cells are assayed for interferon- γ and/or
30 interleukin-12 (or one or more subunits thereof), which may be evaluated by methods known to those of ordinary skill in the art, such as an enzyme-linked immunosorbent assay (ELISA) or, in the case of IL-12 P70 subunit, a bioassay such as an assay measuring proliferation of T cells. In general, a polypeptide that results in the production of at least 50 pg of interferon- γ per mL of cultured supernatant (containing 10^4 - 10^5 T cells per mL) is
35 considered able to stimulate the production of interferon- γ . A polypeptide that stimulates

the production of at least 10 pg/mL of IL-12 P70 subunit, and/or at least 100 pg/mL of IL-12 P40 subunit, per 10^5 macrophages or B cells (or per 3×10^5 PBMC) is considered able to stimulate the production of IL-12.

- In general, immunogenic antigens are those antigens that stimulate proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) in T cells, NK cells, B cells and/or macrophages derived from at least about 25% of *M. tuberculosis*-immune individuals. Among these immunogenic antigens, polypeptides having superior therapeutic properties may be distinguished based on the magnitude of the responses in the above assays and based on the percentage of individuals for which a response is observed.
- 10 In addition, antigens having superior therapeutic properties will not stimulate proliferation and/or cytokine production *in vitro* in cells derived from more than about 25% of individuals who are not *M. tuberculosis*-immune, thereby eliminating responses that are not specifically due to *M. tuberculosis*-responsive cells. Those antigens that induce a response in a high percentage of T cell, NK cell, B cell and/or macrophage preparations from
- 15 *M. tuberculosis*-immune individuals (with a low incidence of responses in cell preparations from other individuals) have superior therapeutic properties.

- Antigens with superior therapeutic properties may also be identified based on their ability to diminish the severity of *M. tuberculosis* infection in experimental animals, when administered as a vaccine. Suitable vaccine preparations for use on experimental animals
- 20 are described in detail below. Efficacy may be determined based on the ability of the antigen to provide at least about a 50% reduction in bacterial numbers and/or at least about a 40% decrease in mortality following experimental infection. Suitable experimental animals include mice, guinea pigs and primates.

25 5.3. ISOLATION OF CODING SEQUENCES

- The present invention also relates to nucleic acid molecules that encode fusion polypeptides of *M. tuberculosis*. In a specific embodiment by way of example in Section 6, *infra*, thirteen *M. tuberculosis* fusion coding sequences were constructed. In accordance with the invention, any nucleotide sequence which encodes the amino acid sequence of the
- 30 fusion protein can be used to generate recombinant molecules which direct the expression of the coding sequence.

- In order to clone full-length coding sequences or homologous variants to generate the fusion polynucleotides, labeled DNA probes designed from any portion of the nucleotide sequences or their complements disclosed herein may be used to screen a
- 35 genomic or cDNA library made from various strains of *M. tuberculosis* to identify the

coding sequence of each individual component. Isolation of coding sequences may also be carried out by the polymerase chain reactions (PCR) using two degenerate oligonucleotide primer pools designed on the basis of the coding sequences disclosed herein.

The invention also relates to isolated or purified polynucleotides complementary to the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25, and polynucleotides that selectively hybridize to such complementary sequences. In a preferred embodiment, a polynucleotide which hybridizes to the sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25 or its complementary sequence under conditions of low stringency and encodes a protein that retains the immunogenicity of the fusion proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 and 26 is provided. By way of example and not limitation, exemplary conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792): Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10⁶ cpm ³²P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and re-exposed to film. Other conditions of low stringency which may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations).

In another preferred embodiment, a polynucleotide which hybridizes to the coding sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25 or its complementary sequence under conditions of high stringency and encodes a protein that retains the immunogenicity of the fusion proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 and 26 is provided. By way of example and not limitation, exemplary conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/mL denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100 µg/mL denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.01%

PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50°C for 45 min before autoradiography. Other conditions of high stringency which may be used are well known in the art.

In yet another preferred embodiment, a polynucleotide which hybridizes to the coding sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23 and 25 or its complementary sequence under conditions of moderate stringency and encodes a protein that retains the immunogenicity of the fusion proteins of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24 and 26 is provided. Exemplary conditions of moderate stringency are as follows: Filters containing DNA are pretreated for 6 h at 55°C in a solution containing 6X SSC, 5X Denhart's solution, 0.5% SDS and 100 µg/mL denatured salmon sperm DNA. Hybridizations are carried out in the same solution and 5-20 X 10⁶ cpm ³²P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 55°C, and then washed twice for 30 minutes at 60°C in a solution containing 1X SSC and 0.1% SDS. Filters are blotted dry and exposed for autoradiography. Other conditions of moderate stringency which may be used are well-known in the art. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.1% SDS.

5.4. POLYPEPTIDES ENCODED BY THE CODING SEQUENCES

In accordance with the invention, a polynucleotide of the invention which encodes a fusion protein, fragments thereof, or functional equivalents thereof may be used to generate recombinant nucleic acid molecules that direct the expression of the fusion protein, fragments thereof, or functional equivalents thereof, in appropriate host cells. The fusion polypeptide products encoded by such polynucleotides may be altered by molecular manipulation of the coding sequence.

Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence, may be used in the practice of the invention for the expression of the fusion polypeptides. Such DNA sequences include those which are capable of hybridizing to the coding sequences or their complements disclosed herein under low, moderate or high stringency conditions described in Sections 5.3, *supra*.

Altered nucleotide sequences which may be used in accordance with the invention include deletions, additions or substitutions of different nucleotide residues resulting in a sequence that encodes the same or a functionally equivalent gene product. The gene product itself may contain deletions, additions or substitutions of amino acid residues, which result in a silent change thus producing a functionally equivalent antigenic epitope.

Such conservative amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine, histidine and arginine; amino acids with uncharged polar head groups having similar hydrophilicity values include the following: glycine, asparagine, glutamine, serine, threonine and tyrosine; and amino acids with nonpolar head groups include alanine, valine, isoleucine, leucine, phenylalanine, proline, methionine and tryptophan.

The nucleotide sequences of the invention may be engineered in order to alter the fusion protein coding sequence for a variety of ends, including but not limited to, alterations which modify processing and expression of the gene product. For example, mutations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, phosphorylation, etc.

In an alternate embodiment of the invention, the coding sequence of a fusion protein could be synthesized in whole or in part, using chemical methods well known in the art. See, e.g., Caruthers *et al.*, 1980, *Nuc. Acids Res. Symp. Ser.* 7:215-233; Crea and Horn, 180, *Nuc. Acids Res.* 9(10):2331; Matteucci and Caruthers, 1980, *Tetrahedron Letter* 21:719; and Chow and Kempe, 1981, *Nuc. Acids Res.* 9(12):2807-2817. Alternatively, the polypeptide itself could be produced using chemical methods to synthesize an amino acid sequence in whole or in part. For example, peptides can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography. (See Creighton, 1983, *Proteins Structures And Molecular Principles*, W.H. Freeman and Co., N.Y. pp. 50-60). The composition of the synthetic polypeptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; see Creighton, 1983, *Proteins, Structures and Molecular Principles*, W.H. Freeman and Co., N.Y., pp. 34-49).

Additionally, the coding sequence of a fusion protein can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis, *in vitro* site-directed mutagenesis (Hutchinson, C., *et al.*, 1978, *J. Biol. Chem* 253:6551), use of TAB® linkers (Pharmacia), and the like. It is important that the manipulations do not destroy immunogenicity of the fusion polypeptides.

In addition, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the sequence. Non-classical amino acids include, but are not limited to, the D-isomers of the common amino acids, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino
5 hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

- 10 In a specific embodiment, the coding sequences of each antigen in the fusion protein are joined at their amino- or carboxy-terminus via a peptide bond in any order. Alternatively, a peptide linker sequence may be employed to separate the individual polypeptides that make-up a fusion polypeptide by a distance sufficient to ensure that each polypeptide folds into a secondary and tertiary structure that maximizes its antigenic
15 effectiveness for preventing and treating tuberculosis. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides;
20 and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea *et al.*, Gene 40:39-46, 1985; Murphy *et al.*, Proc. Natl. Acad. Sci. USA
25 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference. For example, the antigens in a fusion protein may be connected by a flexible polylinker
30 such as Gly-Cys-Gly or Gly-Gly-Gly-Gly-Ser repeated 1 to 3 times (Bird *et al.*, 1988, Science 242:423-426; Chaudhary *et al.*, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:1066-1070).

- In one embodiment, such a protein is produced by recombinant expression of a nucleic acid encoding the protein. Such a fusion product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other
35 by methods known in the art, in the proper coding frame, and expressing the product by

methods known in the art. Alternatively, such a product may be made by protein synthetic techniques, *e.g.*, by use of a peptide synthesizer. Coding sequences for other molecules such as a cytokine or an adjuvant can be added to the fusion polynucleotide as well.

5.5. PRODUCTION OF FUSION PROTEINS

In order to produce a *M. tuberculosis* fusion protein of the invention, the nucleotide sequence coding for the protein, or a functional equivalent, is inserted into an appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. The host cells or cell lines transfected or transformed with recombinant expression vectors can be used for a variety of purposes. These include, but are not limited to, large scale production of the fusion protein.

Methods which are well known to those skilled in the art can be used to construct expression vectors containing a fusion coding sequence and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. (See, *e.g.*, the techniques described in Sambrook et al., 1989, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y. and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y.). RNA capable of encoding a polypeptide may also be chemically synthesized (Gait, *ed.*, 1984, Oligonucleotide Synthesis, IRL Press, Oxford).

5.5.1. EXPRESSION SYSTEMS

A variety of host-expression vector systems may be utilized to express a fusion protein coding sequence. These include, but are not limited to, microorganisms such as bacteria (*e.g.*, *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing a coding sequence; yeast (*e.g.*, *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing a coding sequence; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing a coding sequence; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing a coding sequence; or mammalian cell systems (*e.g.*, COS, CHO, BHK, 293, 3T3 cells). The expression elements of these systems vary in their strength and specificities.

Depending on the host/vector system utilized, any of a number of suitable

transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ , plac, ptrp, ptac (ptrp-lac hybrid promoter; cytomegalovirus promoter) and the like may be used; when cloning in insect cell systems, promoters such as the baculovirus polyhedron promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (e.g., heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll α/β binding protein) or from plant viruses (e.g., the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when generating cell lines that contain multiple copies of a the antigen coding sequence, SV40-, BPV- and EBV-based vectors may be used with an appropriate selectable marker.

Bacterial systems are preferred for the expression of *M. tuberculosis* antigens. For *in vivo* delivery, a bacterium such as *Bacillus-Calmette-Guerrin* may be engineered to express a fusion polypeptide of the invention on its cell surface. A number of other bacterial expression vectors may be advantageously selected depending upon the use intended for the expressed products. For example, when large quantities of the fusion protein are to be produced for formulation of pharmaceutical compositions, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther *et al.*, 1983, EMBO J. 2:1791), in which a coding sequence may be ligated into the vector in frame with the *lacZ* coding region so that a hybrid protein is produced; pIN vectors (Inouye and Inouye, 1985, Nucleic Acids Res. 13:3101-3109; Van Heeke and Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can be purified easily from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned fusion polypeptide of interest can be released from the GST moiety.

5.5.2. PROTEIN PURIFICATION

Once a recombinant protein is expressed, it can be identified by assays based on the

physical or functional properties of the product, including radioactive labeling of the product followed by analysis by gel electrophoresis, radioimmunoassay, ELISA, bioassays, etc.

Once the encoded protein is identified, it may be isolated and purified by standard methods including chromatography (*e.g.*, high performance liquid chromatography, ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. The actual conditions used will depend, in part, on factors such as net charge, hydrophobicity, hydrophilicity, etc., and will be apparent to those having skill in the art. The functional properties may be evaluated using any suitable assay such as antibody binding, induction of T cell proliferation, stimulation of cytokine production such as IL2, IL-4 and IFN- γ . For the practice of the present invention, it is preferred that each fusion protein is at least 80% purified from other proteins. It is more preferred that they are at least 90% purified. For *in vivo* administration, it is preferred that the proteins are greater than 95% purified.

5.6. USES OF THE FUSION PROTEIN CODING SEQUENCE

The fusion protein coding sequence of the invention may be used to encode a protein product for use as an immunogen to induce and/or enhance immune responses to *M. tuberculosis*. In addition, such coding sequence may be ligated with a coding sequence of another molecule such as cytokine or an adjuvant. Such polynucleotides may be used *in vivo* as a DNA vaccine (U.S. Patent Nos. 5,589,466; 5,679,647; 5,703,055). In this embodiment of the invention, the polynucleotide expresses its encoded protein in a recipient to directly induce an immune response. The polynucleotide may be injected into a naive subject to prime an immune response to its encoded product, or administered to an infected or immunized subject to enhance the secondary immune responses.

In a preferred embodiment, a therapeutic composition comprises a fusion protein coding sequence or fragments thereof that is part of an expression vector. In particular, such a polynucleotide contains a promoter operably linked to the coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another embodiment, a polynucleotide contains a coding sequence flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the coding sequence (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra *et al.*, 1989, Nature 342:435-438).

Delivery of the nucleic acid into a subject may be either direct, in which case the subject is directly exposed to the nucleic acid or nucleic acid-carrying vector, or indirect, in

which case, cells are first transformed with the nucleic acid *in vitro*, then transplanted into the subject. These two approaches are known, respectively, as *in vivo* or *ex vivo* gene transfer.

In a specific embodiment, the nucleic acid is directly administered *in vivo*, where it is expressed to produce the encoded fusion protein product. This can be accomplished by any of numerous methods known in the art, *e.g.*, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, *e.g.*, by infection using a defective or attenuated retroviral or other viral vector (*see*, U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (*e.g.*, a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules (United States Patent Nos. 5,407,609; 5,853,763; 5,814,344 and 5,820,883), or by administering it in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (*see, e.g.*, Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432) which can be used to target cell types specifically expressing the receptors, etc. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted *in vivo* for cell specific uptake and expression, by targeting a specific receptor (*see, e.g.*, PCT Publications WO 92/06180 dated April 16, 1992; WO 92/22635 dated December 23, 1992; WO92/20316 dated November 26, 1992; WO93/14188 dated July 22, 1993; WO 93/20221 dated October 14, 1993). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra *et al.*, 1989, Nature 342:435-438).

In a specific embodiment, a viral vector such as a retroviral vector can be used (*see*, Miller *et al.*, 1993, Meth. Enzymol. 217:581-599). Retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. A fusion coding sequence is cloned into the vector, which facilitates delivery of the nucleic acid into a recipient. More detail about retroviral vectors can be found in Boesen *et al.*, 1994, Biotherapy 6:291-302, which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes *et al.*, 1994, J. Clin. Invest. 93:644-651; Kiem *et al.*, 1994, Blood 83:1467-1473; Salmons and Gunzberg, 1993, Human Gene Therapy 4:129-

141; and Grossman and Wilson, 1993, Curr. Opin. in Genetics and Devel. 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for
5 adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Adeno-associated virus (AAV) has also been proposed for use in *in vivo* gene transfer (Walsh *et al.*, 1993, Proc. Soc. Exp. Biol. Med. 204:289-300.

Another approach involves transferring a construct to cells in tissue culture by such
10 methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a subject.

In this embodiment, the nucleic acid is introduced into a cell prior to administration
15 *in vivo* of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the
20 introduction of foreign genes into cells (see *e.g.*, Loeffler and Behr, 1993, Meth. Enzymol. 217:599-618; Cohen *et al.*, 1993, Meth. Enzymol. 217:618-644; Cline, 1985, Pharmac. Ther. 29:69-92) and may be used in accordance with the present invention.

The polynucleotides of the invention may also be used in the diagnosis of tuberculosis for detection of polynucleotide sequences specific to *M. tuberculosis* in a
25 patient. Such detection may be accomplished, for example, by isolating polynucleotides from a biological sample obtained from a patient suspected of being infected with the bacteria. Upon isolation of polynucleotides from the biological sample, a labeled polynucleotide of the invention that is complementary to one or more of the polynucleotides, will be allowed to hybridize to polynucleotides in the biological sample
30 using techniques of nucleic acid hybridization known to those of ordinary skill in the art. For example, such hybridization may be carried out in solution or with one hybridization partner on a solid support.

35 5.7. THERAPEUTIC AND PROPHYLACTIC USES OF THE FUSION PROTEIN

Purified or partially purified fusion proteins or fragments thereof may be formulated as a vaccine or therapeutic composition. Such composition may include adjuvants to enhance immune responses. In addition, such proteins may be further suspended in an oil emulsion to cause a slower release of the proteins *in vivo* upon injection. The optimal ratios of each component in the formulation may be determined by techniques well known to those skilled in the art.

Any of a variety of adjuvants may be employed in the vaccines of this invention to enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Suitable adjuvants are commercially available and include, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, quil A, SBAS1c, SBAS2 (Ling et al., 1997, Vaccine 15:1562-1567), SBAS7 and Al(OH)₃.

In the vaccines of the present invention, it is preferred that the adjuvant induces an immune response comprising Th1 aspects. Suitable adjuvant systems include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MLP) together with an aluminum salt. An enhanced system involves the combination of a monophosphoryl lipid A and a saponin derivative, particularly the combination of 3D-MLP and the saponin QS21 as disclosed in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol as disclosed in WO 96/33739. Previous experiments have demonstrated a clear synergistic effect of combinations of 3D-MLP and QS21 in the induction of both humoral and Th1 type cellular immune responses. A particularly potent adjuvant formation involving QS21, 3D-MLP and tocopherol in an oil-in-water emulsion is described in WO 95/17210 and is a preferred formulation.

Formulations containing an antigen of the present invention may be administered to a subject *per se* or in the form of a pharmaceutical or therapeutic composition. Pharmaceutical compositions comprising the proteins may be manufactured by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Pharmaceutical compositions may be formulated in conventional manner using one or more physiologically acceptable carriers, diluents, excipients or auxiliaries which facilitate processing of the polypeptides into preparations which can be used pharmaceutically. Proper formulation is dependent upon

the route of administration chosen.

For topical administration, the proteins may be formulated as solutions, gels, ointments, creams, suspensions, etc. as are well-known in the art.

Systemic formulations include those designed for administration by injection, *e.g.* subcutaneous, intravenous, intramuscular, intrathecal or intraperitoneal injection, as well as those designed for transdermal, transmucosal, oral or pulmonary administration.

For injection, the proteins may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. The solution may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the proteins may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, a composition can be readily formulated by combining the proteins with pharmaceutically acceptable carriers well known in the art. Such carriers enable the proteins to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a subject to be treated. For oral solid formulations such as, for example, powders, capsules and tablets, suitable excipients include fillers such as sugars, such as lactose, sucrose, mannitol and sorbitol; cellulose preparations such as maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP); granulating agents; and binding agents. If desired, disintegrating agents may be added, such as the cross-linked polyvinylpyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

If desired, solid dosage forms may be sugar-coated or enteric-coated using standard techniques.

For oral liquid preparations such as, for example, suspensions, elixirs and solutions, suitable carriers, excipients or diluents include water, glycols, oils, alcohols, etc.

Additionally, flavoring agents, preservatives, coloring agents and the like may be added.

For buccal administration, the proteins may take the form of tablets, lozenges, etc. formulated in conventional manner.

For administration by inhalation, the proteins for use according to the present invention are conveniently delivered in the form of an aerosol spray from pressurized packs or a nebulizer, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane,

trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the proteins and a suitable powder base such as lactose or starch.

The proteins may also be formulated in rectal or vaginal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the proteins may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the proteins may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Alternatively, other pharmaceutical delivery systems may be employed. Liposomes and emulsions are well known examples of delivery vehicles that may be used to deliver an antigen. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. The fusion proteins may also be encapsulated in microspheres (United States Patent Nos. 5,407,609; 5,853,763; 5,814,344 and 5,820,883). Additionally, the proteins may be delivered using a sustained-release system, such as semipermeable matrices of solid polymers containing the therapeutic or vaccinating agent. Various sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the proteins for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the reagent, additional strategies for protein stabilization may be employed.

Determination of an effective amount of the fusion protein for inducing an immune response in a subject is well within the capabilities of those skilled in the art, especially in light of the detailed disclosure provided herein.

An effective dose can be estimated initially from *in vitro* assays. For example, a dose can be formulated in animal models to achieve an induction of an immune response using techniques that are well known in the art. One having ordinary skill in the art could readily optimize administration to humans based on animal data. Dosage amount and interval may be adjusted individually. For example, when used as a vaccine, the polypeptides and/or polynucleotides of the invention may be administered in about 1 to 3

doses for a 1-36 week period. Preferably, 3 doses are administered, at intervals of about 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *M. tuberculosis* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose range will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

5.8 DIAGNOSTIC USES OF THE FUSION PROTEIN

The fusion polypeptides of the invention are useful in the diagnosis of tuberculosis infection *in vitro* and *in vivo*. The ability of a polypeptide of the invention to induce cell proliferation or cytokine production can be assayed by the methods disclosed in Section 5.2, *supra*.

In another aspect, this invention provides methods for using one or more of the fusion polypeptides to diagnose tuberculosis using a skin test *in vivo*. As used herein, a skin test is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide with dermal cells of the patient, such as, for example, a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least about 48 hours after injection, more preferably about 48 to about 72 hours after injection.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to the test antigen (*i.e.*, the immunogenic portion of the polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 1.0 cm in diameter, is a positive response, indicative of tuberculosis infection, which may or may not be manifested as an active disease.

The fusion polypeptides of this invention are preferably formulated, for use in a skin test, as pharmaceutical compositions containing a polypeptide and a physiologically acceptable carrier. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 µg to about 100 µg, preferably from about

10 µg to about 50 µg in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80™.

In another aspect, the present invention provides methods for using the polypeptides to diagnose tuberculosis. In this aspect, methods are provided for detecting *M. tuberculosis* infection in a biological sample using the fusion polypeptides alone or in combination. As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient or a blood supply. The polypeptide(s) are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to mycobacterial antigens which may be indicative of tuberculosis.

In embodiments in which more than one fusion polypeptide is employed, the polypeptides used are preferably complementary (*i.e.*, one component polypeptide will tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *M. tuberculosis*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more fusion polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested. Such polypeptides are complementary. Approximately 25-30% of sera from tuberculosis-infected individuals are negative for antibodies to any single protein. Complementary polypeptides may, therefore, be used in combination to improve sensitivity of a diagnostic test.

There are a variety of assay formats known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. See, *e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (*e.g.*, in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind

to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. *In* such cases, adsorption may be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1 μ g, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a fusion polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection

reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time is that period of time that is sufficient to detect the presence of antibody within a *M. tuberculosis*-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (for example, Protein A, Protein G, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups, biotin and colloidal particles, such as colloidal gold and selenium. The conjugation of binding agent to reporter group may be achieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (*e.g.* Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent

groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*M. tuberculosis* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for tuberculosis. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., 1985, *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for tuberculosis.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*M. tuberculosis* antibodies in the sample. Typically, the concentration

of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 5 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (e.g., one drop) of patient serum or blood.

The invention having been described, the following examples are offered by way of illustration and not limitation.

6. **EXAMPLE: FUSION PROTEINS OF *M. TUBERCULOSIS* ANTIGENS RETAIN IMMUNOGENICITY OF THE INDIVIDUAL COMPONENTS**

6.1. **MATERIALS AND METHODS**

6.1.1. **CONSTRUCTION OF FUSION PROTEINS**

Coding sequences of *M. tuberculosis* antigens were modified by PCR in order to facilitate their fusion and subsequent expression of fusion protein. DNA amplification was performed using 10 µl 10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at either 70 ng/µl (for TbRa3 antigen) or 50 ng/µl (for 38 kD and Tb38-1 antigens). For TbRa3 antigen, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD antigen, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 antigen, denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for 1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 72°C for 4 min.

Following digestion with a restriction endonuclease to yield the desired cohesive or blunt ends, a polynucleotide specific for each fusion polypeptide was ligated into an expression plasmid. Each resulting plasmid contained the coding sequences of the individual antigens of each fusion polypeptide. The expression vectors used were pET-12b and pT7⁺L2 IL 1.

Three coding sequences for antigens Ra12, TbH9 and Ra35 were ligated to encode one fusion protein (SEQ ID NOS:1 and 2) (Fig. 1A and 2B). Another three coding sequences for antigens Erd14, DPV and MTI were ligated to encode a second fusion protein (SEQ ID NOS:3 and 4) (Fig. 2). Three coding sequences for antigens TbRa3, 38kD and Tb38-1 were ligated to encode one fusion protein (SEQ ID NOS:5 and 6) (Fig. 3A - 3D). Two coding sequences for antigens TbH9 and Tb38-1 were ligated to encode one fusion protein (SEQ ID NOS:7 and 8) (Fig. 4A - 4D). Four coding sequences for antigens TbRa3, 38kD, Tb38-1 and DPEP were ligated to encode one fusion protein (SEQ ID NOS:9 and 10) (Fig. 5A - 5J). Five coding sequences for antigens Erd14, DPV, MTI, MSL and MTCC2 were ligated to encode one fusion protein (SEQ ID NOS:11 and 12) (Fig. 6A and 6B). Four coding sequences for antigens Erd14, DPV, MTI and MSL were ligated to encode one fusion protein (SEQ ID NOS:13 and 14) (Fig. 7A and 7B). Four coding sequences for antigens DPV, MTI, MSL and MTCC2 were ligated to encode one fusion protein (SEQ ID NOS:15 and 16) (Fig. 8A and 8B). Three coding sequences for antigens DPV, MTI and MSL were ligated to encode one fusion protein (SEQ ID NOS:17 and 18) (Fig. 9A and 9B). Three coding sequences for antigens TbH9, DPV and MTI were ligated to encode one fusion protein (SEQ ID NOS:19 and 20) (Fig. 10A and 10B). Three coding sequences for antigens Erd14, DPV and MTI were ligated to encode one fusion protein (SEQ ID NOS:21 and 22) (Fig. 11A and 11B). Two coding sequences for antigens TbH9 and Ra35 were ligated to encode one fusion protein (SEQ ID NOS:23 and 24) (Fig. 12A and 12B). Two coding sequences for antigens Ra12 and DPPD were ligated to encode one fusion protein (SEQ ID NOS:25 and 26) (Fig. 13A and 13B).

The recombinant proteins were expressed in *E. coli* with six histidine residues at the amino-terminal portion using the pET plasmid vector (pET-17b) and a T7 RNA polymerase expression system (Novagen, Madison, WI). *E. coli* strain BL21 (DE3) pLysE (Novagen) was used for high level expression. The recombinant (His-Tag) fusion proteins were purified from the soluble supernatant or the insoluble inclusion body of 500 ml of IPTG induced batch cultures by affinity chromatography using the one step QIAexpress Ni-NTA Agarose matrix (QIAGEN, Chatsworth, CA) in the presence of 8M urea. Briefly, 20 ml of an overnight saturated culture of BL21 containing the pET construct was added into 500 ml of 2xYT media containing 50 µg/ml ampicillin and 34 µg/ml chloramphenicol, grown at 37°C with shaking. The bacterial cultures were induced with 2mM IPTG at an OD₅₆₀ of 0.3 and grown for an additional 3 h (OD = 1.3 to 1.9). Cells were harvested from 500 ml batch cultures by centrifugation and resuspended in 20 ml of binding buffer (0.1 M sodium phosphate, pH 8.0; 10 mM Tris-HCl, pH 8.0) containing 2mM PMSF and 20 µg/ml

leupeptin plus one complete protease inhibitor tablet (Boehringer Mannheim) per 25 ml. *E. coli* was lysed by freeze-thaw followed by brief sonication, then spun at 12 k rpm for 30 min to pellet the inclusion bodies.

The inclusion bodies were washed three times in 1% CHAPS in 10 mM Tris-HCl (pH 8.0). This step greatly reduced the level of contaminating LPS. The inclusion body was finally solubilized in 20 ml of binding buffer containing 8 M urea or 8M urea was added directly into the soluble supernatant. Recombinant fusion proteins with His-Tag residues were batch bound to Ni-NTA agarose resin (5 ml resin per 500 ml inductions) by rocking at room temperature for 1 h and the complex passed over a column. The flow through was passed twice over the same column and the column washed three times with 30 ml each of wash buffer (0.1 M sodium phosphate and 10 mM Tris-HCl, pH 6.3) also containing 8 M urea. Bound protein was eluted with 30 ml of 150 mM imidazole in wash buffer and 5 ml fractions collected. Fractions containing each recombinant fusion protein were pooled, dialyzed against 10 mM TrisHCl (pH 8.0) bound one more time to the Ni-NTA matrix, eluted and dialyzed in 10 mM Tris-HCl (pH 7.8). The yield of recombinant protein varies from 25 - 150 mg per liter of induced bacterial culture with greater than 98% purity. Recombinant proteins were assayed for endotoxin contamination using the *Limulus* assay (BioWhittaker) and were shown to contain < 10 E.U./mg.

20 6.1.2. T-CELL PROLIFERATION ASSAY

Purified fusion polypeptides were tested for the ability to induce T-cell proliferation in peripheral blood mononuclear cell (PBMC) preparations. The PBMCs from donors known to be PPD skin test positive and whose T-cells were shown to proliferate in response to PPD and crude soluble proteins from *M. tuberculosis* were cultured in RPMI 1640 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified polypeptides were added in duplicate at concentrations of 0.5 to 10 µg/ml. After six days of culture in 96-well round-bottom plates in a volume of 200 µl, 50 µl of medium was removed from each well for determination of IFN-γ levels, as described below in Section 6.1.3. The plates were then pulsed with 1 µCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that resulted in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

35 6.1.3. INTERFERON-γ ASSAY

Spleens from mice were removed aseptically and single cell suspension prepared in

complete RPMI following lysis of red blood cells. 100 μ l of cells (2×10^5 cells) were plated per well in a 96-well flat bottom microtiter plate. Cultures were stimulated with the indicated recombinant proteins for 24h and the supernatant assayed for IFN- γ .

The levels of supernatant IFN- γ was analysed by sandwich ELISA, using antibody pairs and procedures available from PharMingen. Standard curves were generated using recombinant mouse cytokines. ELISA plates (Corning) were coated with 50 μ l/well (1 μ g/ml, in 0.1 M bicarbonate coating buffer, pH9.6) of a cytokine capture mAb (rat anti-mouse IFN- γ (PharMingen; Cat. # 18181D)), and incubated for 4 h at room temp. Shake out plate contents and block with PBS-0.05% Tween, 1.0% BSA (200 μ l/well) overnight at 4°C and washed for 6X in PBS-0.1% Tween. Standards (mouse IFN- γ) and supernatant samples diluted in PBS-0.05% Tween, 0.1% BSA were then added for 2 hr at room temp. The plates were washed as above and then incubated for 2 hr at room temperature with 100 μ l/well of a second Ab (biotin rat α mouse IFN- γ (Cat. # 18112D; PharMingen) at 0.5 μ g/ml diluted in PBS-0.05% Tween, 0.1% BSA. After washing, plates were incubated with 100 μ l/well of streptavidin-HRP (Zymed) at a 1:2500 dilution in PBS-0.05% Tween, 0.1% BSA at room temp for 1hr. The plates were washed one last time and developed with 100 μ l/well TMB substrate (3,3',5,5' — tetramethylbenzidine, Kirkegaard and Perry, Gaithersburg, MD) and the reaction stopped after color developed, with H₂SO₄, 50 μ l/well. Absorbance (OD) were determined at 450 nm using 570 nm as a reference wavelength and the cytokine concentration evaluated using the standard curve.

6.2. RESULTS

6.2.1. TRI-FUSION PROTEINS INDUCED IMMUNE RESPONSES

Three coding sequences for *M. tuberculosis* antigens were inserted into an expression vector for the production of a fusion protein. The antigens designated Ra12, TbH9 and Ra35 were produced as one recombinant fusion protein (Figure 1A and 1B). Antigens Erd14, DPV and MTI were produced as a second fusion protein (Figure 2). The two fusion proteins were affinity purified for use in *in vitro* and *in vivo* assays.

The two fusion proteins were tested for their ability to stimulate T cell responses from six PPD⁺ subjects. When T cell proliferation was measured, both fusion proteins exhibited a similar reactivity pattern as their individual components (Figure 14A-14F). A similar result was obtained when IFN- γ production was measured (Figure 15A-15F). For example, subject D160 responded to antigens TbH9 and MTI individually. Subject D160 also responded to the fusion proteins that contained these antigens (Figure 14B and 15B).

In contrast, no T cell response from D160 was observed to other antigens individually. Another subject, D201, who did not react with antigens Erd14, DPV or MTI individually, was also unresponsive to the fusion protein containing these antigens. It should be noted that when the T cell responses to the individual components of the two fusion proteins were not particularly strong, the fusion proteins stimulated responses that were equal to or higher than that induced by the individual antigens in most cases.

The Ra12-TbH9-Ra35 tri-fusion protein was also tested as an immunogen *in vivo*. In these experiments, the fusion protein was injected into the footpads of mice for immunization. Each group of three mice received the protein in a different adjuvant formulation: SBAS1c, SBAS2 (Ling *et al.*, 1997, Vaccine 15:1562-1567), SBAS7 and AL(OH)₃. After two subcutaneous immunizations at three week intervals, the animals were sacrificed one week later, and their draining lymph nodes were harvested for use as responder cells in T cell proliferation and cytokine production assays.

Regardless which adjuvant was used in the immunization, strong T cell proliferation responses were induced against TbH9 when it was used as an individual antigen (Figure 16A). Weaker responses were induced against Ra35 and Ra12 (Figure 16B and 16C). When the Ra12-TbH9-Ra35 fusion protein was used as immunogen, a response similar to that against the individual components was observed.

When cytokine production was measured, adjuvants SBAS1c and SBAS2 produced similar IFN- γ (Figure 17) and IL-4 responses (Figure 18). However, the combination of SBAS7 and aluminum hydroxide produced the strongest IFN- γ responses and the lowest level of IL-4 production for all three antigens. With respect to the humoral antibody response *in vivo*, Figure 19A-19F shows that the fusion protein elicited both IgG₁ and IgG_{2a} antigen-specific responses when it was used with any of the three adjuvants.

Additionally, C57BL/6 mice were immunized with a combination of two expression constructs each containing Ra12-TbH9-Ra35 (Mtb32A) or Erd14-DPV-MTI (Mtb39A) coding sequence as DNA vaccines. The immunized animals exhibited significant protection against tuberculosis upon a subsequent aerosol challenge of live bacteria. Based on these results, a fusion construct of Mtb32A and Mtb39A coding sequences was made, and its encoded product tested in a guinea pig long term protection model. In these studies, guinea pigs were immunized with a single recombinant fusion protein or a mixture of Mtb32A and Mtb39A proteins in formulations containing an adjuvant. Figure 20A-20C shows that guinea pigs immunized with the fusion protein in SBAS1c or SBAS2 were better protected against the development of tuberculosis upon subsequent challenge, as compared to animals immunized with the two antigens in a mixture in the same adjuvant formulation. The fusion

proteins in SBAS2 formulation afforded the greatest protection in the animals. Thus, fusion proteins of various *M. tuberculosis* antigens may be used as more effective immunogens in vaccine formulations than a mixture of the individual components.

5 **6.2.2. BI-FUSION PROTEIN INDUCED IMMUNE RESPONSES**

A bi-fusion fusion protein containing the TbH-9 and Tb38-1 antigens without a hinge sequence was produced by recombinant methods. The ability of the TbH9-Tb38-1 fusion protein to induce T cell proliferation and IFN- γ production was examined. PBMC from three donors were employed: one donor had been previously shown to respond to
10 TbH9 but not to Tb38-1 (donor 131); one had been shown to respond to Tb38-1 but not to TbH9 (donor 184); and one had been shown to respond to both antigens (donor 201). The results of these studies demonstrate the functional activity of both the antigens in the fusion protein (Figures 21A and 21B, 22A and 22B, and 23A and 23B).

15 **6.2.3. A TETRA-FUSION PROTEIN REACTED WITH TUBERCULOSIS PATIENT SERA**

A fusion protein containing TbRa3, 38KD antigen, Tb38-1 and DPEP was produced by recombinant methods. The reactivity of this tetra-fusion protein referred to as TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA. The results of
20 these studies (Table 1) demonstrate that all four antigens function independently in the fusion protein.

One of skill in the art will appreciate that the order of the individual antigens within each fusion protein may be changed and that comparable activity would be expected provided that each of the epitopes is still functionally available. In addition, truncated
25 forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and any clones, nucleotide or amino acid sequences which are functionally equivalent are within the scope
30 of the invention. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. It is also to be understood that all base pair sizes given for nucleotides are approximate and are used for purposes of description.

35 All publications cited herein are incorporated by reference in their entirety.

TABLE 1
REACTIVITY OF TbF-2 FUSION PROTEIN WITH TB AND NORMAL SERA

	Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
							38 kD	TbRa3	Tb38-1	DPEP
5	B931-40	TB	0.57	+	0.321	+	-	+	-	+
	B931-41	TB	0.601	+	0.396	+	+	+	+	-
	B931-109	TB	0.494	+	0.404	+	+	+	±±	-
	B931-132	TB	1.502	+	1.292	+	+	+	+	±±
10	5004	TB	1.806	+	1.666	+	±±	±±	+	-
	15004	TB	2.862	+	2.468	+	+	+	+	-
	39004	TB	2.443	+	1.722	+	+	+	+	-
	68004	TB	2.871	+	2.575	+	+	+	+	-
	99004	TB	0.691	+	0.971	+	-	±±	+	-
	107004	TB	0.875	+	0.732	+	-	±±	+	-
	92004	TB	1.632	+	1.394	+	+	±±	±±	-
	97004	TB	1.491	+	1.979	+	+	±±	-	+
	118004	TB	3.182	+	3.045	+	+	±±	-	-
	173004	TB	3.644	+	3.578	+	+	+	+	-
15	175004	TB	3.332	+	2.916	+	+	+	-	-
	274004	TB	3.696	+	3.716	+	-	+	-	+
	276004	TB	3.243	+	2.56	+	-	-	+	-
	282004	TB	1.249	+	1.234	+	+	-	-	-
	289004	TB	1.373	+	1.17	+	-	+	-	-
	308004	TB	3.708	+	3.355	+	-	-	+	-
	314004	TB	1.663	+	1.399	+	-	-	+	-
	317004	TB	1.163	+	0.92	+	+	-	-	-
20	312004	TB	1.709	+	1.453	+	-	+	-	-
	380004	TB	0.238	-	0.461	+	-	±±	-	+
	451004	TB	0.18	-	0.2	-	-	-	-	±±
	478004	TB	0.188	-	0.469	+	-	-	-	±±
	410004	TB	0.384	+	2.392	+	±±	-	-	+
	411004	TB	0.306	+	0.874	+	-	+	-	+
	421004	TB	0.357	+	1.456	+	-	+	-	+
	528004	TB	0.047	-	0.196	-	-	-	-	+
25	A6-87	Normal	0.094	-	0.063	-	-	-	-	-
	A6-88	Normal	0.214	-	0.19	-	-	-	-	-
	A6-89	Normal	0.248	-	0.125	-	-	-	-	-
	A6-90	Normal	0.179	-	0.206	-	-	-	-	-
	A6-91	Normal	0.135	-	0.151	-	-	-	-	-
	A6-92	Normal	0.064	-	0.097	-	-	-	-	-
	A6-93	Normal	0.072	-	0.098	-	-	-	-	-
	A6-94	Normal	0.072	-	0.064	-	-	-	-	-
30	A6-95	Normal	0.125	-	0.159	-	-	-	-	-
	A6-96	Normal	0.121	-	0.12	-	-	-	-	-
35										
	Cut-off		0.284		0.266					

WHAT IS CLAIMED IS:

1. A purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24, said amino acid sequence may optionally contain one or more conservative amino acid substitutions.
2. A purified polypeptide encoded by a polynucleotide that hybridizes under moderately stringent conditions to a second polynucleotide which is complementary to a nucleotide sequence that encodes the amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22 and 24, said amino acid sequence induces an immune response to *M. tuberculosis*.
3. The polypeptide of Claim 2 which is a soluble polypeptide.
4. The polypeptide of Claim 2 which is produced by a recombinant DNA method.
5. The polypeptide of Claim 2 which is produced by a chemical synthetic method.
6. The polypeptide of Claim 2 which induces an antibody response.
7. The polypeptide of Claim 2 which induces a T cell response.
8. The polypeptide of Claim 2 which is fused with a second heterologous polypeptide.
9. A method of preventing tuberculosis, comprising administering to a subject an effective amount of the polypeptide of Claim 1.
10. A method of preventing tuberculosis, comprising administering to a subject an effective amount of the polypeptide of Claim 2.
11. A method of preventing tuberculosis, comprising administering to a subject an effective amount of a polynucleotide that encodes the polypeptide of Claim 2.

12. A pharmaceutical composition comprising the polypeptide of Claim 2.

13. A pharmaceutical composition comprising a polynucleotide that encodes the polypeptide of Claim 2.

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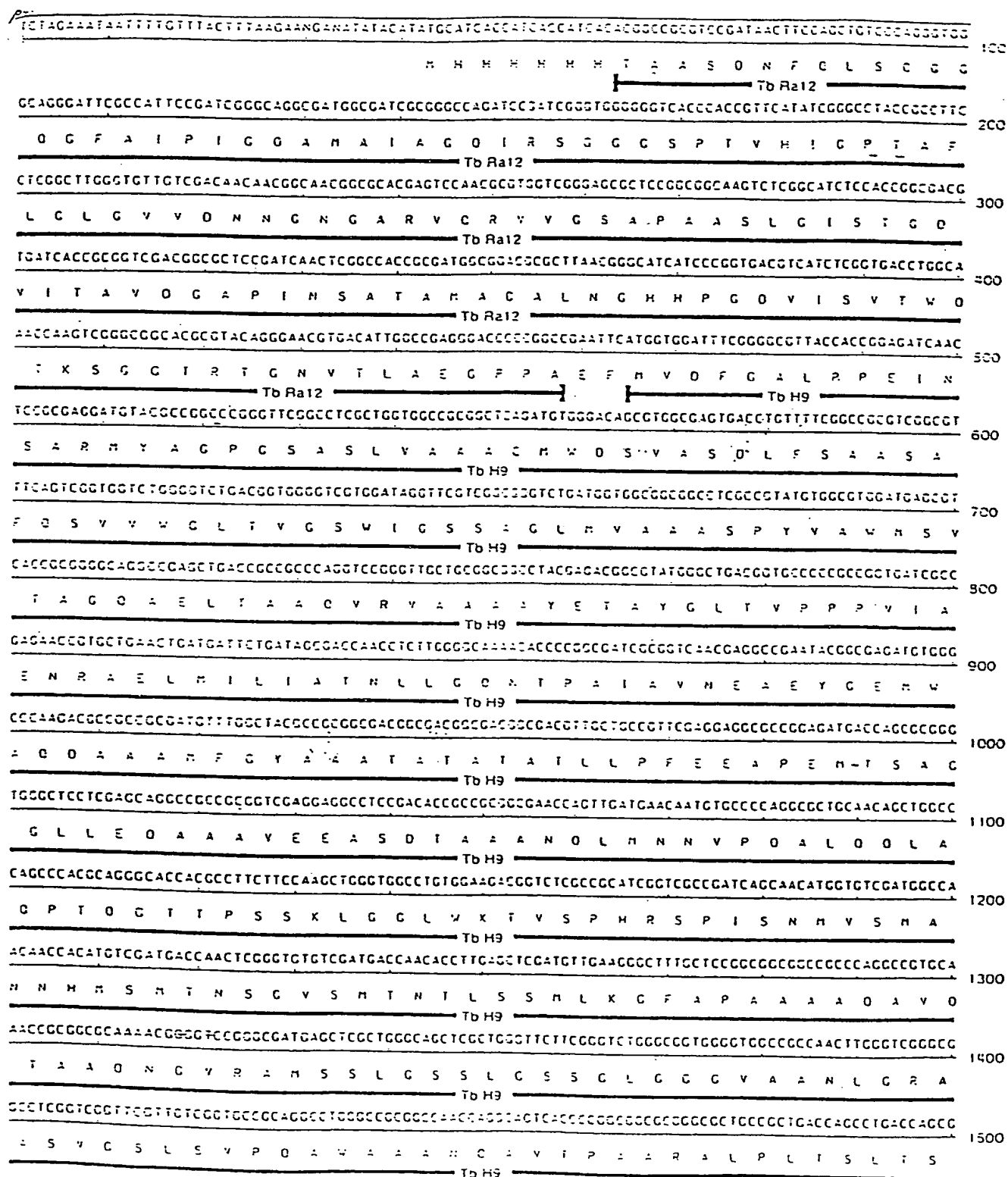


FIG. 1A

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1800
TCCCGGAAAGAGCGCCCGGCCAGATGCTGGCGCGGCTGCGGGTGGGGCAGATGGGCGCAGGGCCCGCTGGTGGGTCAGTGGTGGTGGGCTGCTGGG
A A E R C P G C H L G G L P V C C H C A R A G G G L S G V L R V P P
Tb H9
1700
CCGACCCATATGATGCCGCAATTCCTCGGCAGCGCGCGATATCGCCCGCGCGGCTTGTGCGAGGACCGGTTCGCGCACTTCGCGCGGCTGCGGCTCGAC
R P Y V H P H S P A A G D I A P P A L S O D R F A O F P A L P L D
Tb H9 Tb Ra35
1600
CCGTCCCGGATGGTCCGCCAAGTGGGGCCACAGGTGGTCAACATCAACACCAAATCGGGCTACAACAACGCGGTGGGCGCGCGGACCGGCAJCGJCATCG
P S A H V A O V G P O V V N I N T X L G Y N N A V G A C T G I V I
Tb Ra35
1500
ATCCCAACCGGTGTGCTGCTGACCAACAACCAGTGTATCGCGGGCGCCACCGACATCAATCGGTTACGGGTGGGCTCGGCGCAAACTACGGCGTGGATG
D P N G V V L T N N H V I A G A T D I N A F S V G S G O T Y G V D V
Tb Ra35
2000
GGTGGGTATGACCGCACCCAGGATGTGCGGGTGTGCGAGTGGCGGGTGGCGGTGGGCTACCATCGCGCGGATCGGTGGGCGGCTGGCGGTGGTGG
V G Y D R T O D V A V L O L R G A G G L P S A A I G G C V A V G E
Tb Ra35
2100
CCCTTCCTCGGATGGGCAACAGCGGTGGGCGGGCGGAACGCGCGGTGGGCTGGCAGGGTGGTGGGCTGGGCAAACTGGTGGAGGCGTGGGAT
P F V A H G N S G G O G G T P R A V P G R V Y A L G O T V O A S D
Tb Ra35
2200
CGCTGACCGGTGGCGAAGACATTCGAACGGGTGATCCAGTTCGATCGCGCGATCCAGCGCGGTGATTCGGCGCGGCGGTGCTCAACGGGCTAGGACA
S L T C A E E T L N G L I O F O A A I O P C O S C G P V V N G L C G
Tb Ra35
GGTGGTGGTATGAACAGCGCGCGGTCTAGGATATCCATCAGACTGGCGCGGCTTCGAGCAGATCCCGNTGTAAACAAAGCCCGAAA 2267
V V G H N T A A S
Tb Ra35

FIG 1B

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GATATACATATGCATCACCATCACCATCACATGGCCACCACCCCTTCCCGTTACGGCCACCCCGCGTCCCTTTCCCGGAGTTTCTGAGTTCTTCCGGG 100
M H H H H H H M A T T L P V O R H P R S L F P E F S E L F A
CCTTCCCGTCATTTCGCCGACTCCGGCCACCTTCGACACCCGGTTGATCGCGCTGGAAGACGAGATGAAAGAGGGCGCTACGAGGTACCGCGCGAGCT 200
A F P S F A G L R P T F D T R L H R L E D E M K E G R Y E V R A E L
TCCCGGGTTCGACCCGACAAGGACGTCGACATTATGGTCCGGATGGTCAGCTGACCATCAAGCCGAGCCGACCGAGCAGAAGCACTTCGACGGTCCG 300
P G V O P O X D V O I H V R D G O L T I K A E R T E O X D F D G R
TCGAATTCCGCTACGGTTCTTCGTTCCGACCGGTGTCGCTGCCGGTAGGTCTCAGCAGGACGACATTAAGGCCACCTACGACAAGGGCATTCTTACTG 400
S E F A Y C S F V R T V S L P V G A O E D D I K A T Y O X G I L T
TGTCGGTGGCGTTTCCGAAGGGAAGCCAACCGAAAAGCACATTCAGATCCGCTCCACCAACAAGCTTGATCCCGTGGACGGGTCATTAAACACCACCTG 500
V S V A V S E G K P T E X H I O I R S T N K L D P V O A V I N T T C
CAATTACGGCCAGGTAGTAGCTGCGCTCAACCGGACCGGATCCGGGGCTGCCGCACAGTTCAACCCCTCACCAGGTGGCGGAGTCTATTTCGCCAATTTG 600
N Y G O V V A A L N A T D P C A A A O F N A S P V A O S Y L R N F
CTCCCCCACCAGCCCTCAGCGCGCTGCCATGCCCGCCCAATTGCAAGCTGTCGCCGGCGCGGCACAGTACATCGGCTTGTTCGAGTCGGTTGCCGGCT 700
L A A P P P O R A A H A A O L O A V P G A A O Y I G L V E S V A C
CCTGCAACAACATGAGCTCATGACGATTATTACCACTTCCGGGACGTCACGCTCATGGCGCCATGATCCCGCTCAGCGCGCGTCTCTTCAGCGCGA 800
S C N N Y E L H T I N Y O F G O V O A H G A M I R A O A A S L E A E
CCATCAGGCCATCGTTCTGTATGTCTTGGCCGCGGCTGACTTTTGGGGCGCGCGGTTCCGTTGCTTCCAGGAGTTCATTACCACTTGGCGCGTAAC 900
H O A I V R D V L A A G D F W G C A C S V A C O E F I T O L G R N
TTCCAGGTGATCTACGAGCAGGCAACGCCACGGCCAGAGGCTGCGGCTGCCGCAACAACATGCCGCAACCGACAGCGCGCTCGGCTCCAGCTGCG 1000
F O V I Y E O A N A H G O X V O A A C N N H A O T D S A V C S S V
CCACTAGTAACGGCCCGCAGTGTGCTGCAATTCTGCAGATATCCATCACACTGCCGGCGCGCTCGAGCAGATCCGCTGCTA 1091

ERD 14
ERD 14
ERD 14
ERD 14
ERD 14
HindII
DPV
DPV
MTI
SacI
MTI

A [Sde I]

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FIG. 2.

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TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA
 60
 AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC
 120
 GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG
 172
 Val Lys Ile Arg Leu His Thr
 1 5
 CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC
 220
 Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly
 10 15 20
 TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC
 268
 Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala
 25 30 35
 GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG
 316
 Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu
 40 45 50 55
 ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC
 364
 Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala
 60 65 70
 TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT
 412
 Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly
 75 80 85
 TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG
 460
 Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly
 90 95 100

Fig. 3A

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GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG
 508
 Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly
 105 110 115

CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC
 556
 Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn
 120 125 130 135

CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG
 604
 Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala
 140 145 150

GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT
 652
 Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala
 155 160 165

GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG
 700
 Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu
 170 175 180

CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG
 748
 His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu
 185 190 195

TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC
 796
 Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr
 200 205 210 215

ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC
 844
 Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn
 220 225 230

GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT
 892
 Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr
 235 240 245

Fig. 3 B

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ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG
 940
 Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu
 250 255 260

GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA
 988
 Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln
 265 270 275

AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC
 1036
 Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn
 280 285 290 295

CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC
 1084
 Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile
 300 305 310

ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC
 1132
 Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala
 315 320 325

ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC
 1180
 Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly
 330 335 340

AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC
 1228
 Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro
 345 350 355

GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC
 1273
 Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser
 360 365 370

TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA
 1333

GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG
 1393

Fig. 3c

GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG
1453

AGGCGATGGG TCGGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC
1513

CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA
1573

CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT
1633

CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT
1693

GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG
1753

TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC
1813

TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGCGC GGCGACCCGG GCAACGGGGA
1873

GGGCATGTTG GTGTCCGGTC TGGTGTTGGC GGTGATGGTC GTTCCCATA TCGCCACCAC
1933

CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC
1993

Fig. 3D

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCCGGA TTGAAGTCCA GGTACTCGTG	60
GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT	120
GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC	180
CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCCG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG	420
ACAGCATTCG GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCGG GCTGGTGGCC	600
TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTTGTTT GCGCTCTGGG ATGCGCTCGA CCTCGGCGAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG	900
CCAATGGCGT TGGAGCACAA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCCTGCGA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC	1020
CGTCGCCCCA CGTTGTCTGT GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCCGAGGTC	1080
GTCGCGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGCGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACCAGA CCGAAATCAC AGTGCCCGGC GTGCATTTCTG TTCAGGAGGA CAGCGATGGC	1260

Fig 4A

GTCGTATCGT	GGGCGGGCGC	TCGGCAGCAT	CGGCGACCTG	GGAGCGCTCT	CATTTACGA	1320
GACCAAGAAT	GTGATTTCCG	GCGAAGGCGG	CGCCCTGCTT	GTCAACTCAT	AAGACTTCCT	1380
GCTCCGGGCA	GAGATTCTCA	GGGAAAAGGG	CACCAATCGC	AGCCGCTTCC	TTCGCAACGA	1440
GGTCGACAAA	TATACGTGGC	AGGACAAAGG	TCTTCCTATT	TGCCCAGCGA	ATTAGTCGCT	1500
GCCTTTCTAT	GGGCTCAGTT	CGAGGAAGCC	GAGCGGATCA	CGCGTATCCG	ATTGGACCTA	1560
TGGAACCGGT	ATCATGAAAG	CTTCGAATCA	TTGGAACAGC	GGGGGCTCCT	GCGCCGTCCG	1620
ATCATCCAC	AGGGCTGCTC	TCACAACGCC	CACATGTACT	ACGTGTTACT	AGCGCCCAGC	1680
GCCGATCGGG	AGGAGGTGCT	GGCGCGTCTG	ACGAGCGAAG	GTATAGGCGC	GGTCTTTCAT	1740
TACGTGCCGC	TTCACGATTC	GCCGGCCGGG	CGTCGCT			1777

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TbH-9: protein sequence

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Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1           5           10           15

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
          20           25           30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
          35           40           45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50           55           60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65           70           75           80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
          85           90           95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
          100          105          110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
          115          120          125

Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
          130          135          140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
          145          150          155          160

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
          165          170          175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
          180          185          190

Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr Ala
          195          200          205

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
          210          215          220

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Fig. 4c

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Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240

Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255

Arg Arg Asn Gly Gly Pro Ala
 260

Tb38-1: protein sequence

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 85 90 95

Fig. 4D

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TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC	120
CTTTCTCGCC ACGTTCGCCG GCTTTCCTCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCCCTATCT CGGTCTATTC	360
TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCCTATTGG TTAAAAAATG AGCTGATTTA	420
ACAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTTCAG GTGGCACTTT	480
TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT	600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC	840
AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG	1080
TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG	1260

Fig. 5A

TCGCACCTGA TTGCCCCGACA TTATCGCGAG CCCATTTTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA	1500
GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG	1560
GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAAATAC TGTCCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG	1680
AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTTACCAGT GGCTGCTGCC	1740
AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG	1800
CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC	1860
ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT	1980
CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTGCGGT TTCGCCACCT CTGACTTGAG	2040
CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG	2100
GCCTTTTAC GGTTCCTGGC CTTTGTGCTG CTTTGTGCTC ACATGTTCTT TCCTGCGTTA	2160
TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC	2220
AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG	2280
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA	2340
CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGTATACT CCGCTATCGC TACGTGACTG	2400
GGTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGTCT	2460
GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG	2520
GTTTTACCG TCATCACCGA AACGCGCGAG GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC	2580
GTGAAGCGAT TCACAGATGT CTGCCTGTTT ATCCGCGTCC AGCTCGTTGA GTTTCTCCAG	2640
AAGCGTTAAT GTCTGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCTGTTT	2700

Fig. 5B

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GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTCATG GGGGTAATGA TACCGATGAA	2760
ACGAGAGAGG ATGCTCACGA TACGGGGTTAC TGATGATGAA CATGCCCGGT TACTGGAACG	2820
TTGTGAGGGT AAACAACCTGG CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG CGCTTCGTTA ATACAGATGT AGGTGTTCCA CAGGGTAGCC AGCAGCATCC	2940
TGCGATGCAG ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA	3000
CGAAACACGG AAACCGAAGA CCATTCATGT TGTGTCTCAG GTCGCAGACG TTTTGCAGCA	3060
GCAGTCGCTT CACGTTTCGCT CGCGTATCGG TGATTCATTC TGCTAACCAG TAAGGCAACC	3120
CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC	3180
CATGCCGGCG ATAATGGCCT GCTTCTCGCC GAAACGTTTG GTGGCGGGAC CAGTGACGAA	3240
GGCTTGAGCG AGGGCGTGCA AGATTCCGAA TACCGCAAGC GACAGGCCGA TCATCGTCGC	3300
GCTCCAGCGA AAGCGTCCT CGCCGAAAAT GACCCAGAGC GCTGCCGGCA CCTGTCCTAC	3360
GAGTTGCATG ATAAAGAAGA CAGTCATAAG TCGGGCGACG ATAGTCATGC CCCGCGCCCA	3420
CCGGAAGGAG CTGACTGGGT TGAAGGCTCT CAAGGGCATC GGTGAGATC CCGGTGCCTA	3480
ATGAGTGAGC TAACTTACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA	3540
CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT	3600
TGGGCGCCAG GGTGGTTTTT CTTTTACCA GTGAGACGGG CAACAGCTGA TTGCCCTTCA	3660
CCGCCTGGCC CTGAGAGAGT TGCAGCAAGC GGTCCACGCT GGTTTGCCCC AGCAGGCGAA	3720
AATCCTGTTT GATGGTGGTT AACGGCGGGA TATAACATGA GCTGTCTTCG GTATCGTCGT	3780
ATCCCACTAC CGAGATATCC GCACCAACGC GCAGCCCGGA CTCGGTAATG GCGCGCATTG	3840
CGCCCAGCGC CATCTGATCG TTGGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTCA	3900
GCATTTGCAT GGTGTGTTGA AAACCGGACA TGGCACTCCA GTCGCCTTCC CGTTCCGCTA	3960
TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCCAGACGC AGACGCGCCG	4020
AGACAGAACT TAATGGGCCC GCTAACAGCG CGATTTGCTG GTGACCCAAT GCGACCAGAT	4080
GCTCCACGCC CAGTCGCGTA CCGTCTTCAT GGGAGAAAAT AATACTGTTG ATGGGTGTCT	4140

Fig. 5c

GGTCAGAGAC ATCAAGAAAT AACGCCGGA CATTAGTGCA GGCAGCTTCC ACAGCAATGG	4200
CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC GCGAGAAGAT	4260
TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTT TACCATCGAC ACCACCACGC	4320
TGGCACCCAG TTGATCGGCG CGAGATTAA TCGCCGCGAC AATTTGCGAC GCGCGTGCA	4380
GGGCCAGACT GGAGGTGGCA ACGCCAATCA GCAACGACTG TTTGCCCGCC AGTTGTTGTG	4440
CCACGCGGTT GGAATGTAA TTCAGCTCCG CCATCGCCGC TTCCACTTTT TCCCGCGTTT	4500
TCGCAGAAAC GTGGCTGGCC TGGTTCACCA CGCGGAAAC GGTCTGATAA GAGACACCGG	4560
CATACTCTGC GACATCGTAT AACGTTACTG GTTTCACATT CACCACCCTG AATTGACTCT	4620
CTTCCGGGCG CTATCATGCC ATACCGCGAA AGGTTTTGCG CCATTTCGATG GTGTCCGGGA	4680
TCTCGACGCT CTCCCTTATG CGACTCCTGC ATTAGGAAGC AGCCCAGTAG TAGGTTGAGG	4740
CCGTTGAGCA CCGCCGCCGC AAGGAATGGT GCATGCAAGG AGATGGCGCC CAACAGTCCC	4800
CCGGCCACGG GGCCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG	4860
CGAGCCCGAT CTTCCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG	4920
GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA	4980
AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA	5040
TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCACGTGAT	5100
CGACATCATC GGGACCAGCC CCACATCCTG GGAACAGGCG GCGGCGGAGG CGGTCCAGCG	5160
GGCGCGGGAT AGCGTCGATG ACATCCGCGT CGCTCGGGTC ATTGAGCAGG ACATGGCCGT	5220
GGACAGCGCC GGCAAGATCA CCTACCGCAT CAAGCTCGAA GTGTCGTTCA AGATGAGGCC	5280
GGCGCAACCG AGGGGCTCGA AACCACCGAG CGGTTGCGCT GAAACGGGCG CCGGCGCCGG	5340
TACTGTCGCG ACTACCCCCG CGTCGTCGCC GGTGACGTTG GCGGAGACCG GTAGCACGCT	5400
GCTCTACCCG CTGTTCAACC TGTGGGGTCC GGCCTTTCAC GAGAGGTATC CGAACGTCAC	5460
GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CCGGGACGGT	5520
CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT	5580

Fig. 5D

GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAAC TACAACCTGC CCGGAGTGAG 5640
CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAAC 5700
CTGGGACGAC CCGCAGATCG CTGCGCTCAA CCCCGGCGTG AACCTGCCCCG GCACCGCGGT 5760
AGTTCCGCTG CACCGCTCCG ACGGGTCCGG TGACACCTTC TTGTTACCC AGTACCTGTC 5820
CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCGGCTTC GGCACCACCG TCGACTTCCC 5880
GGCGGTGCCG GGTGCGCTGG GTGAGAACGG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940
GACACCGGGC TCGGTGGCCT ATATCGGCAT CAGCTTCCTC GACCAGGCCA GTCAACGGGG 6000
ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTC TTGTTGCCCCG ACGCGCAAAG 6060
CATTAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTTCGAT 6120
GATCGACGGG CCCGCCCGG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180
CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGCGAG GCATTTCTGC ACTGGGCGAT 6240
CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTTCAT TTCCAGCCGC TGCCGCCCGC 6300
GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTC AGCGCTGAGA TGAAGACCGA 6360
TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTCGAGCGG ATCTCCGGCG ACCTGAAAAC 6420
CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC 6480
GGGGACGGCC GCCCAGGCCG CGGTGGTGCG CTTCCAAGAA GCAGCCAATA AGCAGAAGCA 6540
GGAACCTCGAC GAGATCTCGA CGAATATTCG TCAGGCCGGC GTCCAATACT CGAGGGCCGA 6600
CGAGGAGCAG CAGCAGGCGC TGTCCTCGCA AATGGGCTTT GTGCCACAA CGGCCGCCTC 6660
GCCGCCGTCG ACCGCTGCAG CGCCACCCGC ACCGGCGACA CCTGTTGCCC CCCCACCACC 6720
GGCCGCCGCC AACACGCCGA ATGCCCAGCC GGGCGATCCC AACGCAGCAC CTCCGCCGGC 6780
CGACCCGAAC GCACCGCCGC CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT 6840
CGACAACCCG GTTGAGGAT TCAGCTTCGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC 6900
CGCCCACTTC GACTACGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTCC 6960
CGGACAGCCG CCGCCGGTGG CCAATGACAC CCGTATCGTG CTCGGCCGGC TAGACCAAAA 7020

Fig. 5 E

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GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT	7080
GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA	7140
CGCCAACGGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA	7200
GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAACG CACCGGACGC	7260
CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAACC CGGTGGACAA	7320
GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCCTTTG GTCGCCCCGC CGCCGGCGCC	7380
GGCACC GGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCCG GCCGGGGAAG TCGCTCCTAC	7440
CCCGACGACA CCGACACCGC AGCGGACCTT ACCGGCCTGA GAATTCTGCA GATATCCATC	7500
ACACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC	7560
CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCTTGG	7620
GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGA ACTATAT CCGGAT	7676

Fig. 5F

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Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	1	5	10	15
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	20	25	30	
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	35	40	45	
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val	50	55	60	
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser	65	70	75	80
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	85	90	95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	100	105	110	
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	115	120	125	
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	130	135	140	
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	145	150	155	160
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	165	170	175	
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	180	185	190	
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	195	200	205	
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	210	215	220	

Fig. 5G

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Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
 225 230 235 240
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
 245 250 255
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
 260 265 270
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
 275 280 285
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
 290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480

Fig 5 H

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Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735

Fig. 5 I

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
740 745 750

Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
755 760 765

Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
770 775 780

Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
785 790 795 800

Pro Ala

Frg. 5J

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CAIATGCATCACCATCACCATCACATGGCCACCACCTTCCCGTTCAGCGCCACCCGGTCCCTCTTCCCGAGTTTCTGAGCTGTTCCGGCCCTTCCCGTCATTCGCGGACTCCGG 120
GTATACGTAGTGGTAGTGGTAGTGTACCGGTGGTGGGAAGGGCAAGTCGGGTGGGCGCCAGGGAGAGGGGCTCAAAAGACTCGACAAGCGCGGAAGGGCAGTAAGCGGCTGAGGCC
Met / HIS TAG Erd 14
H M H H H H H H H A T T L P V O R H P R S L F P E F S E L F A A F P S F A G L R
CCCACCTTCGACACCCGGTTCATCGGGTCCGAAGACGAGATGAAAGAGGGGGCTACGAGGTACGCGCGGAGCTTCCCGGGTCCGACCCGACAAGGACGTCGACATTATGGTCCCGAT 240
GGGTGAAGCTGTGGGCCAACTACGCGGACCTTCGCTCTACTTTCTCCCGCGGATGCTCCATGCGCGCTCGAAGGGCCCGAGCTGGGGCTGTCTCGAGCTGTAATACAGGGCGTA
Erd 14
P T F D T R L M R L E D E M K E G R Y E V R A E L P G V D P O K D V D I H V R D
GGTCAGCTGACCATCAAGGCGAGCGGACCGAGCAGAAGGACTTCGACGGTGGTTCGGAATTCGGGTACGGTTCCTTCGTTCCGACGGTGTGCTGCCGTAGGTGCTGACGAGGACGAC 360
CCAGTCGACTGGTAGTTCGGCTCGGTCGGTGGTCTGCTTCTGAGCTGCCAGCGAGCTTAAGCGCATGCCAAGGAAGCAAGCGTGCACAGCGACGGCATCCAGACTGCTCTGCTG
Erd 14
G O L T I K A E R T E O K D F D G R S E F A Y G S F V R T V S L P V G A D E D D
ATTAAGGCCACCTACGACAAGGGCATTCTTACTGTGTCGGTGGCGGTTTCGGAAGGGAAGCCAACCGAAAAGCACATTAGATCCGGTCCACCAACAAGCTTGATCCCGTGGACGGGTC 480
TAATTCGGTGGATGCTGTTCGGTAAGAATGACACAGCCACCGCAAGGCTTCCTTCGGTGGCTTTTCGTGAAGTCTAGGCGAGGTGGTGTTCGAAGTACGGCACCTGCGCCAG
Erd 14 HindIII DPV
I K A T Y D K G I L T V S V A V S E G K P T E K H I O I R S T N K L D P V D A V
ATTAACACCACTGCAATTACGGCGAGGTAGTACCTGCGCTCAACGGCGAGGATCGGGGGCTGCCGCAGTTCACCGCTCACCGGTGGCGGAGTCTATTTCGCAATTTCCTCGCC 600
TAATGTGGTGGACGTTAATGCCGTCATCATCGACGGAGTTGCGCTGCGTAGGCCCGGACGGGTGTCAGTTGCGGAGTGGCCACCGGTCAGGATAAAGCGTTAAAGGAGCGG
DPV
I N T T C N Y G O V V A A L N A T D P G A A A O F N A S P V A O S Y L R N F L A
GCACGCCACCTCAGCGCGCTGCCATGGCGCGCAATTGCAAGCTGTGCGGGGGGGCGACAGTACATCGGCTTGTGAGTGGTTCGGCGCTCTGCAACAATATGAGCTCATGAGC 720
CGTGGCGGTGGAGTGGCGGACGGTACCGCGCGTTAAGCTTCGACACGGCCCCCGCGTGTATGAGCGGAACAGCTCAGCCAACGGCGGAGGACGTTGTTGATACCTGAGTACTGC
DPV SacI MTI
A P P P O R A A M A A O L O A V P G A A O Y I G L V E S V A G S C N N Y E L M T
ATTAATTACCACTCGGGGACGTCGACGCTCATGGCGCATGATCGCGCTCAGGCGGGTGGCTTGAGCGGAGCATCAGGCCATGTTCTGATGTGTTGGCGCGGGTGAATTTGG 840
TAATTAATGGTCAAGCCCCGAGCTGCGAGTACCGCGGTAC TAGCGCGAGTCCGCGCAGCGAAGTCCGCTCGTAGTCCGGTAGCAAGCACTACACAACCGGCGCCACTGAAAAC
MTI
I N Y D F G D V D A H G A M I R A O A A S L E A E H O A I V R D V L A A G D F W
GGCGCGCGGGTTCGGTGGCTTCCAGGAGTTCATTACCGAGTGGCGCGTAACCTCCAGGTGATCTACGAGCAGGCCAACGCCACGGCGAGAGGTGCGGCGCAACAACATG 960
CCGCGCGGGCAAGCCACCGAAGGTCCTCAAGTAATGGGTCAACCGCGATTGAAGGTCCACTAGATGCTCGTCCGTTGCGGGTGGCGGTCTTCAGCTCCGAGCGCGCTTGTGTAC
MTI
G C A G S V A C O E F I T O L G R N F O V I Y E O A N A H G O K V O A A G N N M
GGCGAAACCGACAGCGCGCTCGGCTCCAGCTGGGCGCACTAGTATGAGCCTTTTGGATGCTCATATCCACAGTTGGTGGCTCCGAGTCCGCGTTTGGCGCAAGCGGGGCTGATCGG 1080
CGCGTTTGGCTGTCGGCGGACCGAGGTGACCCGGTGATCATACTCGAAACCTACGAGTATAGGGTGTCAACCAACCGGAGGTCAGCGCAACCGGGGTTCCGCGCGAGTACGCC
MTI Spel MSL
A O T D S A V G S S V A T S H S L L D A H I P O L V A S O S A F A A K A G L M R
CACACGATCGGTGAGGCGGAGCGGCGGATGTCGGTCAAGCGGTTTACCAGGGGAGTCTGCGCGGGCTTTCAGGCGCGCCATGCGCGGTTTGTGGCGCGCGCGCCAAAGTCAAC 1200
GTGTGTAGCCAGTCCGGTCTGTCGGCGGTACAGCGGATCCGCAAGTGGTCCCTTCAGCAGCGCGCGCAAGTCCGCGGGTACGGGCAACACCGCGCGCGGTTTCAAGTTG
MSL
H T I G O A E O A A M S A D A F H O G E S S A A F O A A H A R F V A A A A K V N
ACCTTGTTCGATGTCGGCGGAGCGGAATCTGGGTGAGCGCGCGGTACCTATGTGGCGCGGATGCTGCGCGCGGTCGACCTATACCGGTTTCGATATCATGATTTTCGGGCTTTTACCT 1320
TGGAAACACCTACAGCGCGTCCGCTTAGACCCACTCCGCGCGCATGATACCGCGGCTACGACCGCGCGGAGTGGATATGGCCCAAGCTATAGTACCTAAAGCCGAAATGGA
MSL RV mTCC2
T L L D V A O A N L G E A A G I Y V A A D A A A A S T Y T G F D I H D F G L L P

Fig. 6A

[illegible]

Fig. 6 B

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CATATGCATCACCATCACCATCACATGGCCACCACCTTCCCGTTCAGCGCCACC CGGGTCCCTCTTCCCGAGTTTCTGAGCTGTTGCGGGCCTTCC 10
GTATACGTAGTGGTAGTGGTAGTGTACCGGTGGTGGGAAGGGCAAGTCGCGGTGGCGCCAGGGAGAAGGGGCTCAAAGACTCGACAAGCGCCGGAAGG
H M H H H H H H M A T T L P V O R H P R S L F P E F S E L F A A F
CGTCATTGCGCGGACTCCGGCCACCTTCGACACCCGGTTGATGCGGCTGGAAGACGAGATGAAAGAGGGGCGCTACGAGGTACGCGCGGAGCTTCCCGG 20
GCAGTAAGCGGCTGAGGCGGGTGGGAAGCTGTGGGCCAACTACGCCGACCTTCTGCTCTACTTTCTCCCGCGATGCTCCATGCGCGCTCGAAGGGCC
P S F A G L R P T F D T R L M R L E D E M K E G R Y E V R A E L P G
GGTCGACCCCGACAAGGACGTCGACATTATGGTCCGCGATGGTCAGCTGACCATCAAGGCCGAGCGCACCGAGCAGAAGGACTTCGACGGTCGCTCGGAA 30
CCAGCTGGGGCTGTTCTCGAGCTGTAATACCAGGCGCTACCACTGCACTGGTAGTTCCGGCTCGCGTGGCTCGTCTTCTGAAGCTGCCAGCGAGCCTT
V D P D K D V D I M V R D G O L T I K A E R T E O K D F O G R S E
TTCGGTACGGTTCCTTCGTTCCGACGGTGTGCTGCCGGTAGGTGCTGACGAGGACGACATTAAGGCCACCTACGACAAGGGCATTCTTACTGTGTGG 40
AAGCGCATGCCAAGGAAGCAAGCGTGCCACAGCGACGGCCATCCACGACTGCTCTGCTGTAATTCGGTGGATGCTGTTCCCGTAAGAATGACACAGCC
F A Y G S F V R T V S L P V G A D E D D I K A T Y D K G I L T V S
TGGCGGTTTEGGAAGGGAAGCCAACCGAAAAGCACATTAGATCCGGTCCACCAACAAGCTTGATCCCGTGGACGCGGTTCATTAACACCACCTGCAATTA 50
ACCGCCAAAGCCTTCCCTTCGGTTGGCTTTTCGTGTAAGTCTAGGCCAGGTGGTGTTCGAAGTAGGGCACCTGCGCCAGTAATTGTGGTGGACGTTAAT
V A V S E G K P T E K H I O I R S T N K L D P V D A V I N T T C N Y
CGGGCAGGTAGTAGCTGCGCTCAACGCGACGGATCCGGGGGCTGCCGACAGTTCAACGCCCTACCGGTGGCGCAGTCTATTTGCGCAATTTCTCGCC 60
GCCCGTCCATCATCGACGCGAGTTGCGCTGCCCTAGGCCCGGACGGCGTGTCAAGTTGCGGAGTGCCACCGCGTCAGGATAAACGCGTTAAAGGAGCGG
G O V V A A L N A T D P G A A A O F N A S P V A O S Y L R N F L A
GCACCGCCACCTCAGCGCGCTGCCATGGCCGCGCAATTGCAAGCTGTGCCGGGGGCGGCACAGTACATCGGCCTTGTGAGTCGCTTGGCGGCTCCTGCA 70
CGTGGCGGTGGAGTCGCGCGACGGTACCGCGCGTTAACGTTTCACACGCGCCCGCGGTGTCATGTAGCCGGAACAGCTCAGCCAACGCGCGAGGACGT
A P P P O R A A H A A O L O A V P G A A O Y I G L V E S V A G S C
ACAACTATGAGCTCATGACGATTAATTACCAGTTCGGGGACGTCGACGCTCATGGCCCATGATCCGCGCTCAGGCGGCGTGGCTTGAGGCGGAGCATCA 80
TGTGATACTCGAGTACTGCTAATTAATGGTCAAGCCCCCTGCAGCTGCGAGTACCGCGGTACTAGGCGCGAGTCCGCCGAGCGAACTCCGCCTCGTAGT
N N Y E L M T I N Y O F G D V D A H G A M I R A O A A S L E A E H O
GGCCATCGTTCGTGATGTGTTGGCCGCGGGTGACTTTTGGGGCGGCGCGGTTCCGTGGCTTGGCAGGAGTTCATTACCCAGTTGGGCGGTAACCTCCAG 90
CCGGTAGCAAGCACTACACAACCGGCGCCCACTGAAAACCCCGCGCGGCCAAGCCACCGAAGGTCCTCAAGTAATGGGTCAACCCGCGATTGAAGGTC
A I V R D V L A A G D F W G G A G S V A C O E F I T O L G R N F O

Fig. 7A

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GTGATCTACGAGCAGGCCAACGCCACGGGCAGAAAGGTGCAGGCTGCCGGCAACAACATGGCGCAAACCGACAGCGCCGTCGGCTCCAGCTGGGCCACTA
CACTAGATGCTCGTCCGGTTGCGGGTGCCCGTCTTCCACGTCCGACGGCCGTTGTTGTACCGCGTTTGGCTGTGCGGGCAGCCGAGGTGCA¹⁰CCCGGTGAT
V I Y E O A N A H G O K V O A A G N N M A O T D S A V G S S W A T
GTATGAGCCTTTTGGATGCTCATATCCACAGTTGGTGGCCTCCAGTCGGCGTTTGCCGCCAAGGCGGGGTGATGCGGCACACGATCGGTCAGGCCGA
CATACTCGGAAAACCTACGAGTATAGGGTGTCAACCACCGGAGGGTCAGCCGCAAACGGCGGTTCCGCCCGACTACGCCGTGTGCTAGCCAGTCCGGCT
S M S L L D A H I P O L V A S O S A F A A K A G L M R H T I G O A E
GCAGGCGGCGATGTCGGCTCAGGCGTTTACCAGGGGGAGTCGTGCGCGGCGTTTCAGGCGCGCCATGCCCGGTTTGTGCGGGCGGCGCCAAAGTCAAC
CGTCCGCCGCTACAGCCGAGTCCGCAAAGTGGTCCCCCTCAGCAGCCGCCGCAAAGTCCGGCGGGTACGGGCCAAACACCGCCGCCGGCGGTTTCAGTTG
O A A M S A O A F H O G E S S A A F O A A H A R F V A A A A K V N
ACCTTGTTGGATGTCGCGCAGGCGAATCTGGGTGAGGCGCGCGGTACCTATGTGGCCGCGGATGCTGCGGCCGCGTCGACCTATACCGGGTTCGATATC
TGGAACAACCTACAGCGCGTCCGCTTAGACCCACTCCGGCGGCCATGGATACACGGCGGCTACGACGCCGGCGCAGCTGGATATGGCCCAAGCTATAG
T L L D V A O A N L G E A A G T Y V A A D A A A A S T Y T G F D I¹²

Fig. 7B

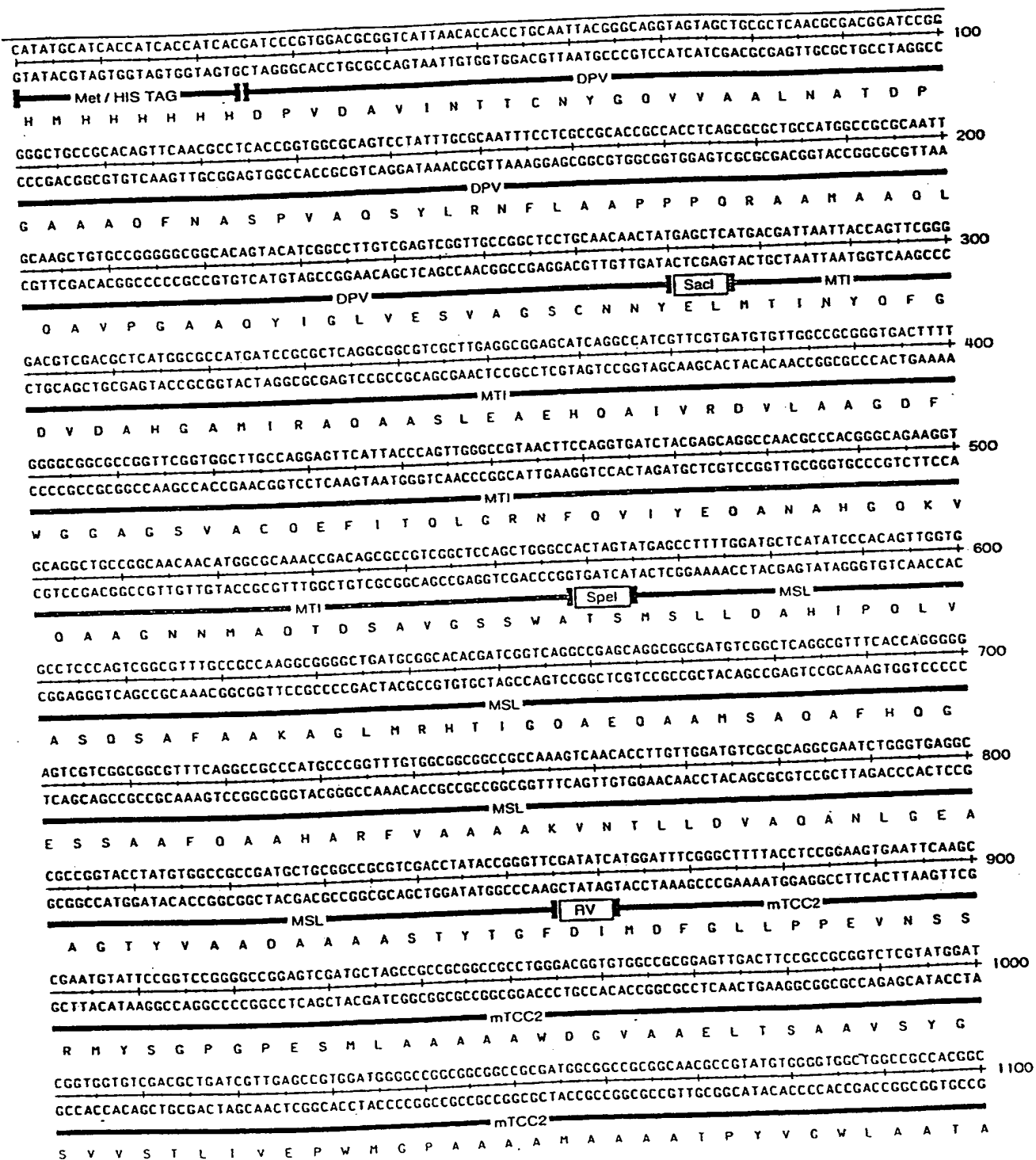


Fig. 8A

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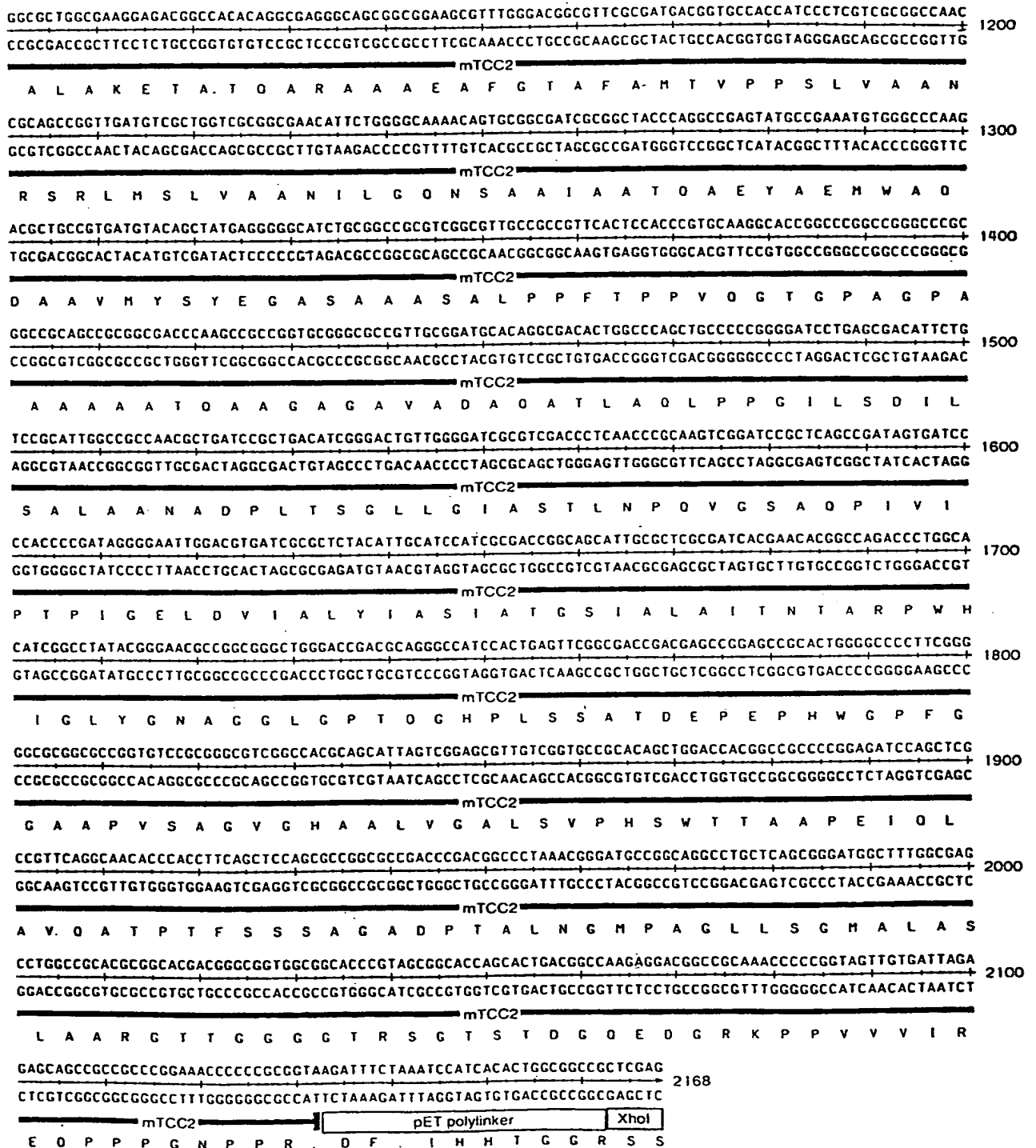


Fig. 8B

CATATGCATCACCATCACCATCAGCATCCCGTGGACGCGGTCATTAACACCACCTGCAATTACGGGCAGGTAGTAGCTGCGCTCAACGCGACGGATCCGG
GTATACGTAGTGGTAGTGGTAGTGCTAGGGCACCTGCGCCAGTAATTGTGGTGGACGTTAATGCCCGTCCATCATCGACGCGAGTTGCGCTGCCTAGGCC
H M H H H H H D P V D A V I N T T C N Y G O V V A A L N A T D P
GGGCTGCCGCACAGTTCAACGCCTCACCGGTGGCGCAGTCCTATTTGCGCAATTTCTCGCCGCACCGCCACCTCAGCGCGCTGCCATGGCCGCGCAATT
CCCGACGCGGTGTCAAGTTGCGGAGTGGCCACCGCGTCAGGATAAACCGGTTAAAGGAGCGGCGTGGCGGTGGAGTCGCGCGACGGTACCGGCGCGTTAA
G A A A O F N A S P V A O S Y L R N F L A A P P P O R A A M A A O L
GCAAGCTGTGCCGGGGGCGGCACAGTACATCGGCCTTGTGAGTCGGTTGCCGGCTCTGCAACAACATGAGCTCATGACGATTAATTACCAGTTCCGGG
CGTTCGACACGGCCCCCGCGGTGTATGTAGCCGGAACAGCTCAGCCAACGGCCGAGGACGTTGTTGATACTCGAGTACTGCTAATTAATGGTCAAGCCC
O A V P G A A O Y I G L V E S V A G S C N N Y E L M T I N Y O F G
GACGTCGACGCTCATGGCGCCATGATCCGCGCTCAGGCGGCGTGGCTTGAGGCGGAGCATCAGGCCATCGTTCGTGATGTGTTGGCCGCGGGTGACTTTT
CTGACGTCGAGTACCGCGGTACTAGGCGCGAGTCCGCGCAGCGAACTCCGCTCGTAGTCCGCTAGCAAGCACTACACAACCGGCGCCCACTGAAAA
D V D A H G A M I R A O A A S L E A E H O A I V R D V L A A G D F
GGGGCGGCGCGGTTTCGGTGGCTTGCCAGGAGTTCATTACCCAGTTGGGCGTAACCTCCAGGTGATCTACGAGCAGGCCAACGCCACGGGCGAGAAGGT
CCCCGCGCGGCCAAGCCACCGAACGGTCTCAAGTAATGGGTCAACCGGCAATTGAAGGTCCACTAGATGCTCGTCCGGTTGCGGGTGCCCGTCTTCCA
W G G A G S V A C O E F I T O L G R N F O V I Y E O A N A H G O K V
GCAGGCTGCCGGCAACAACATGGCGCAAACCGACAGCGCGCTCGGCTCCAGCTGGGCCACTAGTATGAGCCTTTTGGATGCTCATATCCACAGTTGGTG
CGTCCGACGCGCGTTGTTGTACCGCGTTTGGCTGTGCGGCGAGCGAGGTGACCCGGTGATCATACTCGGAAAACCTACGAGTATAGGGTGTCAACCAC
O A A G N N M A O T D S A V G S S W A T S M S L L D A H I P O L V
GCCTCCAGTCGGCGTTTGGCGCAAGGCGGGGCTGATGCGGCACACGATCGGTACGGCCGAGCAGGCGGCGATGTGCGGCTCAGGCGTTTACCAGGGGG
CGGAGGGTCAGCCGCAAACGGCGGTTCCGCCCCGACTACGCCGTGTGCTAGCCAGTCCGGCTCGTCCGCGCTACAGCCGAGTCCGCAAAGTGGTCCCC
A S O S A F A A K A G L M R H T I G O A E O A A M S A O A F H O G
AGTCGTGGCGGCGTTTTCAGGCCGCCCATGCCCGTTTGTGCGGCGGCGCCAAAGTCAACACCTTGTGGATGTCGCGCAGGCGAATCTGGGTGAGGC
TCAGCAGCGCGCAAAGTCCGGCGGTACGGGCCAAACACCGCGCGCGGTTTCAGTTGTGGAACAACCTACAGCGCGTCCGCTTAGACCCACTCCG
E S S A A F O A A H A R F V A A A A K V N T L L D V A O A N L G E A
CGCCGGTACCTATGTGGCCGCGATGCTGCGGCGCGCTCGACCTATACCGGTTTCGATATCCATCACACTGGCGGCGGCTCGAGCAGATCCGGCTGCTAA
GCGGCCATGGATACACCGCGGCTACGACGCGGCGCAGCTGGATATGGCCAAAGTATAGGTAGTGTGACCGCGGCGGAGCTCGTCTAGGCCGACGATT
A G T Y V A A D A A A A S T Y T G F D I H H T G G R S S R S G C

Fig. 9A

CAAAGCCCGAAAGGAAGCTGA
-----> 921
GTTTCGGGCTTTCCTTCGACT

O S P K G S
----->

Fig. 9B

CATATGCATCACCATCACCATCACATGGTGGATTTTCGGGGCGTTACACCGGAGATCAACTCCGCGAGGATGTACGCCGGCCCGGGTTCGGCTCGCTGG 10
GTATACGTAGTGGTAGTGGTAGTGTACCACCTAAAGCCCCGAATGGTGGCTCTAGTTGAGGCGCTCCTACATGCCGCCGGGCCAAGCCGGAGCGACC
H M H H H H H H M V D F G A L P P E I N S A R M Y A G P G S A S L
TGGCCGCGGCTCAGATGTGGACAGCGTGGCGAGTGACCTGTTTTTCGGCCGCGTCGGCGTTTCAGTCGGTGGTCTGGGGTCTGACGGTGGGGTCTGGAT 20
ACCGGGCGCGAGTCTACACCTGTGCGACCGCTCACTGGACAAAAGCCGGCGCAGCCGCAAAGTCAGCCACCAGACCCAGACTGCCACCCAGCACCTA
V A A A O M W D S V A S D L F S A A S A F O S V V W G L T V G ' S W I
AGGTTCTGTCGGCGGGTCTGATGGTGGCGGGCGCTCGCCGTATGTGGCGTGGATGAGCGTCACCGCGGGGCGAGCCGAGCTGACCGCCGCCAGGTCCGG 30
TCCAAGCAGCGCCAGACTACCACCGCCGCGGAGCGGCATACCCGCACCTACTCGAGTGGCGCCCGTCCGGCTGACTGGCGGGGGTCCAGGCC
G S S A G L M V A A A S P Y V A W H S V T A G O A E L T A A O V R
GTTGCTGGCGCGGCTACGAGACGGCGTATGGGCTGACGGTGGCCCCGCGGTCATCGCCGAGAACCCTGCTGAACGTATGATTCTGATAGCGACCAACC 40
CAACGACGCCCGCGGATGCTCTGCCGCATACCCGACTGCCACGGGGCGGGCCACTAGCGGCTCTTGGCACGACTTGACTACTAAGACTATCGCTGGTTGG
V A A A A Y E T A Y G L T V P P P V I A E N R A E L M I L I A T N
TCTTGGGGCAAACACCCCGCGCATCGCGGTCAACGAGGCCGAATACGGCGAGATGTGGGCCAAGACGCCCGCGCATGTTTGGCTACGCCGCGCGCGAC 50
AGAACCCCGTTTTGTGGGGCGCTAGCGCCAGTTGCTCCGGCTTATGCGGCTCTACACCCGGGTTCTGCGGGCGCGCTACAAACCGATGCGGCGCGCGT
L L G O N T P A I A V N E A E Y G E M W A O D A A A M F G Y A A A T
GGCGACGGCGACGGCGACGTTGCTGCCGTTTCGAGGAGGCGCCGGAGATGACCAGCGCGGGTGGGCTCCTCGAGCAGGCCGCCGGTTCGAGGAGGCTCC 60
CCGCTGCCGCTGCCGCTGCAACGACGGCAAGCTCTCCGGGCTCTACTGGTCGCGCCACCCGAGGAGCTCGTCCGGCGGGCCAGCTCTCCGGAGG
A T A T A T L L P F E E A P E M T S A G G L L E O A A A V E E A S
GACACCGCCGCGGCGAACCAGTTGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCACGCCACGAGGGCACCACGCCCTTCTTCAAGCTGGGTG 7
CTGTGGCGGGCGCGCTTGGTCAACTACTTGTACACGGGTCCGCGACGTTGTGACCGGGTCCGGTGGTCCCGTGGTGGGAAGAAGGTTCCGACCCAC
D T A A A N O L H N N V P O A L O O L A O P T O G T T P S S K L G
GCCTGTGAAGACGGTCTCGCCGATCGGTGCGCGATCAGCAACATGGTGTGATGGCCAACAACCATGTGATGACCAACTCGGGTGTGTGATGAC 8
CGGACACCTTCTGCCAGAGCGCGTAGCCAGCGGCTAGTCGTTGTACACAGCTACCGGTTGTTGGTGTACAGCTACTGGTTGAGCCACACAGCTACTG
G L W K T V S P H R S P I S N M V S M A N N H M S M T N S G V S M T
CAACACCTTGAGCTCATGTTGAAGGGCTTTGCTCCGGCGGGCGGGCCAGGCGGTGCAAAACCGCGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTG 9
GTTGTGGAACCTGAGCTACAACTTCCGAAACGAGGCGCGCGCGGGTCCGGACGTTTGGCGCGCGTTTTGCCCGAGGCCGCTACTCGAGCGAC
N T L S S M L K G F A P A A A A O A V O T A A O N G V R A M S S L

Fig. 10A

BGCAGCTCGCTGGGTTCTTCGGGTCTGGGCGGTGGGGTGGCCGCCAACTTGGGTGGGGCGGCTCGGTGGTTGCTTGTGGTGGCGAGGCCTGGGCCG 10
CCGTGAGCGACCCAAGAAGCCAGACCCGCCACCCACCGCGGTGAACCCAGCCCGCGGAGCCAGCCAAGCAACAGCCACGGCGTCCGGACCCGGC
G S S L G S S G L G G G V A A N L G R A A S V G S L S V P O A W A
GGCCAAACAGGCAGTCACCCCGGCGCGGGCGCTGCCGTGACCAGCCTGACCAGCGCCGGAAGAGGGGCCGGCAGATGCTGGGCGGGCTGCC 11
GCCGGTTGGTCCGTGAGTGGGGCGCGCGCCCGGACCGCGACTGGTGGACTGGTGGCGCGCCTTTCTCCCGGGCCGCTACGACCCGCCCGACGG
A A N O A V T P A A R A L P L T S L T S A A E R G P G O M L G G L P
GGTGGGCAGATGGGCGCCAGGGCCGGTGGTGGGCTCAGTGGTGTGCTGCGTGTTCGCCCGGACCCCTATGTGATGCCGATTCTCCGGCAGCCGGCAAG 12
CCACCCCGTCTACCCCGGTCCCGGCCACCCCGAGTCACCACAGCAGCACAAGGCGGCGCTGGGATACCTACGGCGTAAGAGGCCGTCCGGCGTTCC
V G O M G A R A G G G L S G V L R V P P R P Y V M P H S P A A G K
CTTGATCCCGTGGACGCGGTTCATTAAACACCACCTGCAATTACGGGCGAGTAGTAGCTGCGCTCAACGCGACGGATCCGGGGCTGCCGCACAGTTCAACG 13
GAACTAGGGCACCTGCGCCAGTAATTGTGGTGGACGTTAATGCCCGTCCATCATCGACGCGAGTTGCGCTGCCTAGGCCCCCGACGGCGTGTCAAGTTGC
L D P V D A V I N T T C N Y G O V V A A L N A T D P G A A A O F N
CCTCACCGGTGGGCGAGTCCTATTTGCGCAATTTCTCGCCGACCCGCCACCTCAGCGCGCTGCCATGGCCGCGCAATTGCAAGCTGTGCCGGGGCGGC 14
GGAGTGGCCACCGCGTCAGGATAAACCGGTAAAGGAGCGGCGTGGCGGTGGAGTGGCGGACGGTACCGGCGCGTTAACGTTGACACAGGCCCGCCGCCG
A S P V A O S Y L R N F L A A P P P O R A A M A A O L O A V P G A A
ACAGTACATCGGCCTTGTCGAGTCGGTTGCCGGCTCCTGCAACAATATGAGCTCATGACGATTAATTACCAGTTCGGGGACGTCGACGCTCATGGCGCC 15
TGTCATGTAGCGGAACAGTCAGCCAACGGCCGAGGACGTTGTTGATACTCGAGTACTGCTAATTAATGGTCAAGCCCTGCAGCTGCGAGTACCGCGG
O Y I G L V E S V A G S C N N Y E L M T I N Y O F G O V D A H G A
ATGATCCGCGCTCAGGCGGCGTGGCTTGAGGCGGAGCATAGGCCATCGTTGCTGATGTGTTGGCCGCGGGTGACTTTTGGGGCGGCGCGGTTCCGGTGG 16
TACTAGGCGCGAGTCCGCGCAGCGAACTCCGCTCGTAGTCCGGTAGCAAGCACTACACAACCGGCGCCACTGAAAACCCCGCGCGGCAAGCCACC
M I R A O A A S L E A E H O A I V R D V L A A G D F W G G A G S V
CTTGCCAGGAGTTTATTACCCAGTTGGGCGTAACCTCCAGGTGATCTACGAGCAGGCCAACGCCACGGGCGAGAAGGTGCAGGCTGCCGCGCAACAACAT 17
GAACGGTCTCAAGTAATGGTCAACCCGGCATTGAAGGTCCACTAGATGCTCGTCCGGTTGCGGGTGCCCGTCTTCCACGTCCGACGGCGGTTGTTGTA
A C O E F I T O L G R N F O V I Y E O A N A H G O K V O A A G N N M
GGCGCAAACCGACAGCGCGCTCGGCTCCAGCTGGGCCACTAGTAACGGCCGCGAGTGTGCTGGAATTTGCGAGATATCCATCACACTGGCGGCGGCTCGAG 18
CCGCGTTTGGCTGTGCGGCGAGCGGAGTGCACCCGGTGATCATTGCCGGCGGTACACGACCTTAAGACGCTATAGGTAGTGTGACCCCGCGCGAGCTC
A O T D S A V G S S W A T S N G R O C A C I L O I S I T L A A A R

CATATGCATCACCATCACCATCACATGGCCACCACCCTTCCGTTACGCGCCACCCGCGGTCCCTCTTCCCGAGTTTTCTGAGCTGTTGCGGCGCTTCC 10C
GTATACGTAGTGGTAGTGGTAGTGTACCGGTGGTGGGAAGGGCAAGTGCAGGTGGCGCCAGGGAGAAGGGCTCAAAAGACTCGACAAGCGCCGGAAGG
H M H H H H H M A T T L P V O R H P R S L F P E F S E L F A A F
CGTCATTGCGCGGACTCCGGCCACCTTCGACACCCGGTTGATGCGGTGGAAGACGAGATGAAAGAGGGGCGCTACGAGGTACGCGCGGAGCTTCCCGG 20C
GCAGTAAGCGGCTGAGGCGGGTGGAAAGCTGTGGGCCAACTACGCGGACCTTCTGCTCTACTTTCTCCCGGATGCTCCATGCGCGCTCGAAGGGCC
P S F A G L R P T F D T R L M R L E D E M K E G R Y E V R A E L P G
GGTCGACCCCGACAAGGACGTGACATTATGGTCCGGATGGTCAGCTGACCATCAAGGCCGAGCGCACCGAGCAGAAGGACTTCGACGGTCGCTCGGAA 30C
CCAGCTGGGGCTGTTCTCTGAGCTGTAATACCAGGCGCTACCACTGCACTGGTAGTTCGGCTCGGTGGCTCGTCTTCTGAAGCTGCCAGCGAGCCTT
V D P D K D V D I M V R D G O L T I K A E R T E O K D F D G R S E
TTCGCTACGGTTCCTTCGTTGCGACGGTGTGCTGCCGGTAGGTGCTGACGAGGACGACATTAAGGCCACCTACGACAAGGGCATTCTTACTGTGTGCG 40C
AAGCGCATGCCAAGGAAGCAAGCGTGCCACAGCGACGGCCATCCAGCACTGCTCTGCTGTAATTCGGTGGATGCTGTTCCCGTAAGAATGACACAGCC
F A Y G S F V R T V S L P V G A D E D D I K A T Y D K G I L T V S
TGGCGGTTTCGGAAGGGAAGCCAACCGAAAGCACATTCAGATCCGGTCCACCAACAAGCTTGATCCCGTGGACGCGGTCTTAACACCACCTGCAATTA 50
ACCGCCAAAGCCTTCCCTTCGGTTGGCTTTTCGTGTAAGTCTAGGCCAGGTGGTTGTTGCAACTAGGGCACCTGCGCCAGTAATTGTGGTGGACGTTAAT
V A V S E G K P T E K H I O I R S T N K L D P V D A V I N T T C N Y
CGGGCAGGTAGTAGCTGCGCTCAACGCGACGGATCCGGGGCTGCCGACAGTTCAACGCCTACCGGTGGCGCAGTCTTATTGCGCAATTCCTCGCC 60C
GCGGCTCCATCATCGACGCGAGTTGCGCTGCTAGGCCCCGACGGCGTGTCAAGTTGCGGAGTGGCCACCGCGTCAGGATAAACCGGTAAAGGAGCGG
G O V V A A L N A T D P G A A A O F N A S P V A O S Y L R N F L A
GCACCGCCACCTCAGCGCGCTGCCATGGCCGCGCAATTGCAAGCTGTGCCGGGGGGGCGACAGTACATCGGCCTTGTCGAGTGGTTGCCGGCTCTCGCA 70C
CGTGGCGGTGGAGTCCGCGACGGTACCGGCGGTAAAGCTGACACGCGCCCCGCGGTGTCATGTAGCCGGAACAGCTCAGCCAACGCGCGAGGACGT
A P P P O R A A H A A O L O A V P G A A O Y I G L V E S V A G S C
ACAACTATGAGCTCATGACGATTAATTACAGTTTCGGGGACGTGACGCTCATGGGCCATGATCCGCGCTCAGGCGCGTGGCTTGAGGCGGAGCATCA 80C
TGTGATACTCGAGTACTGCTAATTAATGGTCAAGCCCCCTGCAGCTGCGAGTACCGCGGTACTAGGCGCGAGTCCGCGCAGCGAACTCCGCTCGTAGT
N N Y E L M T I N Y O F G O V D A H G A M I R A O A A S L E A E H O
GGCCATCGTTGCTGATGTGTTGGCCGCGGTGACTTTTGGGGCGGGCGCGGTTCGGTGGCTTGCCAGGAGTTCATTACCCAGTTGGGCGGTAACCTCCAG 90C
CCGGTAGCAAGCACTACACAACCGGCGCCACTGAAAACCCGCGCGGCCAAGCCACCGAACGGTCTCAAGTAATGGGTCAACCCGCGATTGAAGGTC
A I V R D V L A A G D F W G G A G S V A C O E F I T O L G R N F O

Fig 11A

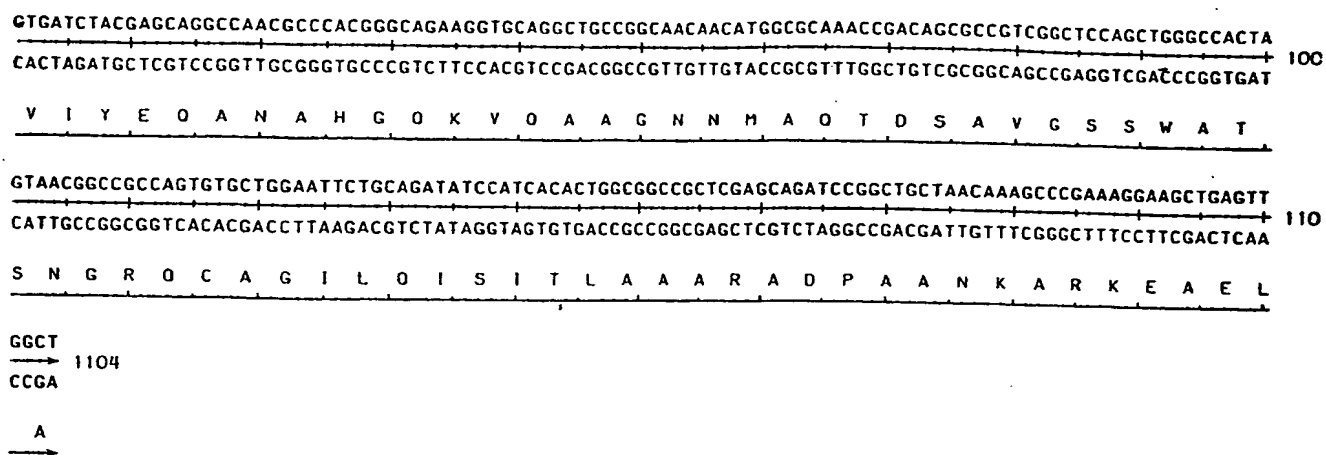


Fig. 11B

CATATGCATCACCATCACCATCACATGGTGGATTTCGGGGCGTTACCACCGAGATCAACTCCGCGAGGATGTACGCCGGCCCGGGTTTCGGECTCGCTGG 100
GTATACGTAGTGGTAGTGGTAGTGACCACCTAAAGCCCCGCAATGGTGGCCTCTAGTTGAGGCGCTCCTACATGCGGCCGGGCCCAAGCCGGAGCGACC
H M H H H H H H H V D F G A L P P E I N S A R M Y A G P G S A S L
TGGCCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTTTCCGGCCGCTCGGCGTTTCAGTCGGTGGTCTGGGGTCTGACGGTGGGGTCTGGAT 200
ACCGGCCGCGAGTCTACACCTGTGCGACCGCTCACTGGACAAAAGCCGGCGCAGCCGCAAGTCAGCCACCAGACCCAGACTGCCACCCAGCACCTA
V A A A Q M W D S V A S D L F S A A S A F O S V V W G L T V G S W I
AGGTCGTGCGGGGTCTGATGGTGGCGGGGCTCGCCGTATGTGGCGTGGATGAGCGTCACCGCGGGCAGGCCGAGCTGACCGCCGCCAGGTCCGG 300
TCCAAGCAGCGCCAGACTACCACCGCCGCGGAGCGGCATACACCGACCTACTCGCAGTGGCGCCCGCTCGGCTCGACTGGCGGGGGTCCAGGCC
G S S A G L M V A A A S P Y V A W M S V T A G O A E L T A A O V R
TTGCTGCGGCGGCTACGAGACGGGTATGGGCTGACGGTGGCCCGCCGGTGTGCGCGAGAACCCTGCTGAACTGATGATTCTGATAGCGACCAACC 400
CAACGACCGCGCGGATGCTCTGCCGCATACCCGACTGCCACGGGGCGGCCACTAGCGGCTCTGGCACGACTTGACTACTAAGACTATCGCTGGTTGG
V A A A A Y E T A Y G L T V P P P V I A E N R A E L M I L I A T N
TCTTGGGGCAAAACACCCCGCGATCGCGGTCAACGAGGCCGAATACGGCGAGATGTGGGCCCAAGACGCCCGCCGATGTTTGGCTACGCCCGCGCGAC 500
AGAACCCCGTTTGTGGGGCGCTAGCGCCAGTTGCTCCGGTTATGCCGCTCTACACCCGGGTTCTGCGGCGGCGCTACAAACCGATGCGGCGCCGCTG
L L G O N T P A I A V N E A E Y G E M W A O O A A A H F G Y A A A T
GGCGACGGCGACGGCGACGTTGCTGCCGTTGAGGAGGCGCGGAGATGACCAGCGCGGTGGGCTCCTCGAGCAGGCCCGCCGGTTCGAGGAGGCTCC 600
CCGCTGCCGCTGCCGCTGCAACGACGGCAAGCTCCTCCGCGGCTCTACTGGTGGCGCCACCCGAGGAGCTCGTCCGGCGGCGCAGCTCCTCCGGAGG
A T A T A T L L P F E E A P E M T S A G G L L E O A A A V E E A S
GACACCGCCGGCGCAACCACTGATGAACAATGTGCCCCAGGCGCTGCAACAGCTGGCCAGCCACGCGAGGGCACCACGCTTCTTCCAAGCTGGGTG 700
CTGTGGCGGCGCGCTTGGTCAACTACTTGTACACGGGTCGCGACGTTGTGACCGGGTGGGTGCGTCCCGTGGTGGGAAGAAGGTTCCAGCCAC
D T A A A N O L H N N V P O A L O O L A O P T O G T T P S S K L G
GCCTGTGAAGACGGTCTCGCCGATCGGTGCGCGATCAGCAACATGGTGTGATGGCCAACAACCATGTGATGACCAACTCGGGTGTGTGATGAC 800
CGGACACCTTCTGCCAGAGCGGGTAGCCAGCGGCTAGTCTGTGTACACAGTACCGGTTGTGTGGTGTACAGCTACTGGTTGAGCCACACAGCTACTG
G L W K T V S P H R S P I S N M V S M A N N H M S M T N S G V S M T
CAACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCCGGCGGGCGGCCAGGCCGTGCAAAACCGGGCGCAAAACGGGGTCCGGGGATGAGCTCGCTG 900
GTTGTGGAACCTCAGCTACAACTTCCGAAACGAGGCCGCGCGGGGTCGGCACGTTTGGCGCCGCTTTTGGCCAGGCCCGCTACTCGAGCGAC
N T L S S M L K G F A P A A A A O A V O T A A O N G V R A M S S L

Fig. 12 A

GGCAGCTCGCTGGGTTCTTCGGGCTGCGGCGGTGGGGTGGCGGCCAACTTGGGTGGGCGGCCCTGGTGGGTTCTGTGGTGGCGCAGGCCTGGGCGG 100
CCGTGAGCGACCCAAGAAGCCAGACCCGCCACCCACCGCGGTGAACCCAGCCCGCGGAGCCAGCAAGCAACAGCCACGGCGTCCCGACCCGGG
G S S L G S S G L G G G V A A N L G R A A S V G S L S V P Q A W A
CGGCCAACAGGCAGTCACCCCGGCGGCGGGGCTGCCGTGACCAGCCTGACCAGCGCCGCGGAAAGAGGGCCCGGCAGATGCTGGGCGGGCTGCC 110
GCCGGTTGGTCCGTAGTGGGCGCGCCCGCCGCGGCGGACTGGTCGGACTGGTCGCGCGCCTTTCTCCGGGCGCGTCTACGACCCGCGCGGAGCG
A A N O A V T P A A R A L P L T S L T S A A E R G P G Q H L G G L P
GGTGGGCGAGATGGGCGCCAGGGCCGGTGGTGGGCTCAGTGGTGTGCTGCGTGTTCGCCGCGACCCATGTGATGCCGATTCTCCGGCAGCGCGGAT 120
CCACCCGCTTACCCGCGGTCCCGGCCACCCGAGTCACACACGACGCACAAGCGCGCGCTGGGATACACTACGGCGTAAGAGGCGGTGGGCGGCTA
V G Q M G A R A G G G L S G V L R V P P R P Y V M P H S P A A G D
ATCGCCCCGCGGCTTGTGCGAGGACCGGTTGCGCGACTTCCCCGCGCTGCCCTCGACCCGTCGCGATGGTGGCCCAAGTGGGGCCACAGGTGGTCA 130
TAGCGGGGCGGCGGAACAGCGTCTTGCCCAAGCGGCTGAAGGGGCGGACGGGGAGCTGGCGAGGCGTACCAGCGGTTACCCCGGTGTCCACCACT
I A P P A L S O D R F A D F P A L P L D P S A M V A O V G P Q V V
ACATCAACACCAAACTGGGCTACAACAACCGGTGGGCGCGGGACCGGCATCGTCATCGATCCCAACGGTGTGCTGCTGACCAACAACACGTGATCGC 140
TGATGTTGTGTTTGACCCGATGTTGTTGCGGCACCCGCGGCCCTGGCGGTAGCAGTAGCTAGGGTTGCCACAGCAGCACTGGTGTGTTGGTGCCTAGCG
N I N T K L G Y N N A V G A G T G I V I D P N G V V L T N N H V I A
GGGCGCCACCGACATCAATGCGTTACGCGTGGGCTCCGGCCAAACCTACGGCGTCGATGTGGTGGGTATGACCGCACCCAGGATGTGCGGTGCTGCAG 150
CCCGCGGTGGCTGTAGTTACGCAAGTCGACCGGAGGCGGTTTGGATGCCGAGCTACACAGCCATACTGGCGTGGGTCTACAGCGCCACGACGTC
G A T D I N A F S V G S G O T Y G V D V V G Y D R T Q D V A V L Q
CTGCGCGGTGCCGTGGCTGCCGTGCGCGCGGATCGGTGGGCGGCTGCGGTTGGTGAGCCCGTCTGCGGATGGGCAACAGCGGTGGGCGAGGCGGAA 160
GACGCGCCACGGCCACCGACGGCAGCGCGCTAGCCACCGCGGACGCGCAACCACTCGGGCAGCAGCGCTACCCGTTGTGCGCCACCGTCCCGCCTT
L R G A G G L P S A A I G G G V A V G E P V V A H G N S G G O G G
CGCCCCGTGGGTGCTTGGCAGGGTGGTGGGCTCGGCCAAACCGTGCAGGCGTGGATTGCTGACCGGTGCCGAAGAGACATTGAACGGGTGATCCA 170
GCGGGGACGCGACGACCGTCCACACGCGGAGCGGTTTGGCACGTCCGACGCTAAGCGACTGGCCACGGCTTCTCTGTAACCTGCCCACTAGGT
T P R A V P G R V V A L G O T V O A S D S L T G A E E T L N G L I O
GTTGATGCCGCGATCCAGCCCGGTGATTGGGCGGGCCGTCGTCAACGGCTAGGACAGGTGGTGGTATGAACACGGCCGCTCCTAGGATATC 1797
CAAGCTACGGCGCTAGGTGGGCGCACTAAGCCCGCCCGGCGAGCAGTTGCCGATCTGTCCACAGCCATACTTGTGCGGCGCAGGATCTATAG
F D A A I O P C D S G G P V V N G L G O V V G M N T A A S O I

Fig. 12B

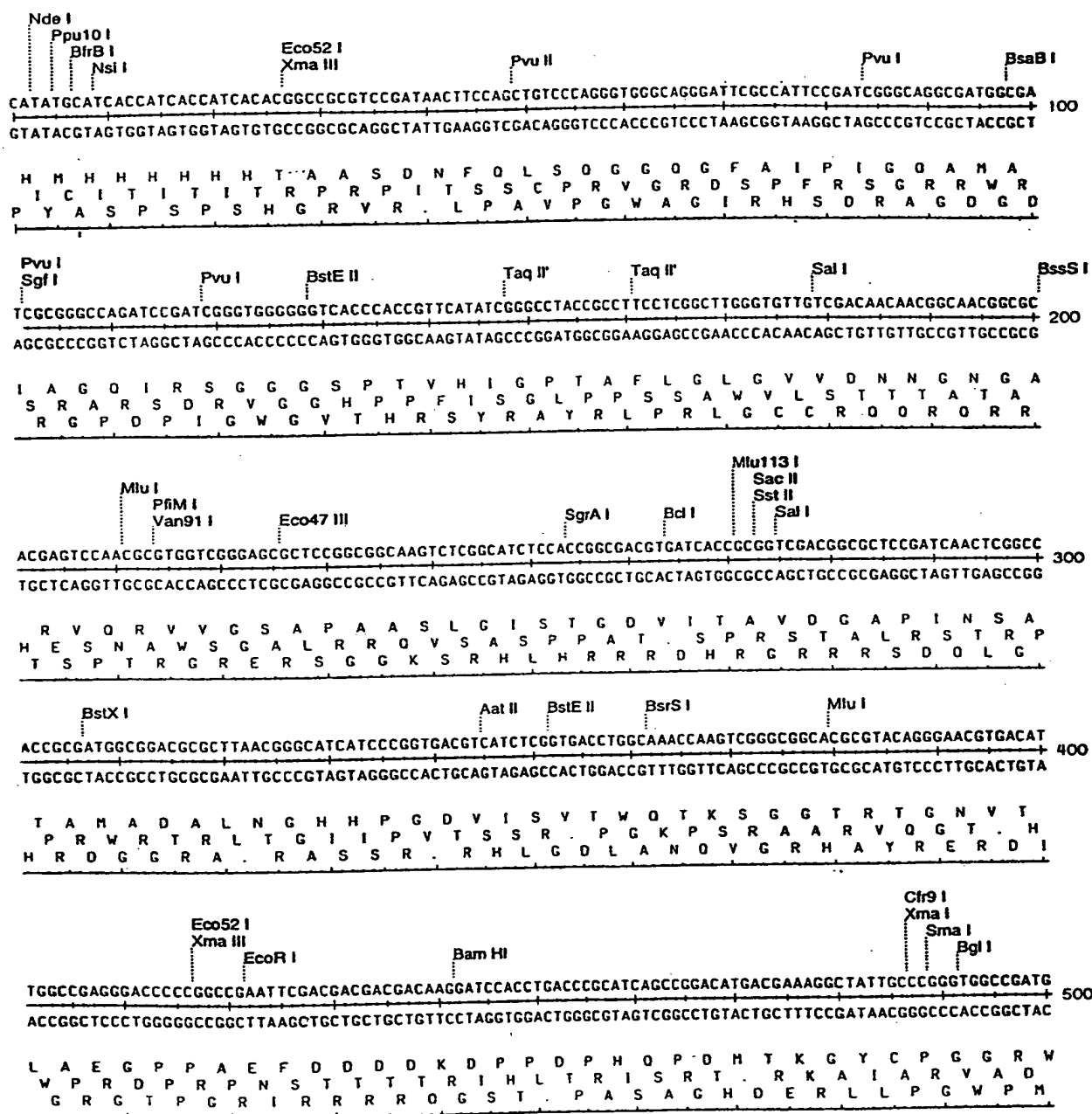


Fig. 13A

GGGTTTGGCGACTTGCCGCTGTCGACGGCGAGAAGTACCCGACGGCTCGTTTGGCACCAGTGGATGCAAACTGGTTTACCGCCACAGTTTAC
CCCAAACCGCTGAACCGGCACACGCTGCCGCTCTTCATGGGGCTGCCGAGCAAAACCGTGGTCACCTACGTTTGCACCAATGGCCGGGTGTCAAAATG 600

G F G D L A V C D G E X Y P D G S F W H O W M O T W F T G P O F Y
G V L A T W P C A T A R S T P T A R F G T S G C K R G L P A H S F T
G F W R L G R V R R R E V P R R L V L A P V D A N V V Y R P T V L

[illegible]

F D C V S G G E P L P G P P P P G G C G G A I P S E Q P N A P . E
S I V S A A V S P S P A R R H R V V A V G O F R P S S P T L P E N
L R L C O R R . A P P R P A A T G W L R W G N S V R A A O R S L R I

TC
→ 702
AG

F
S

Fig. 13 B

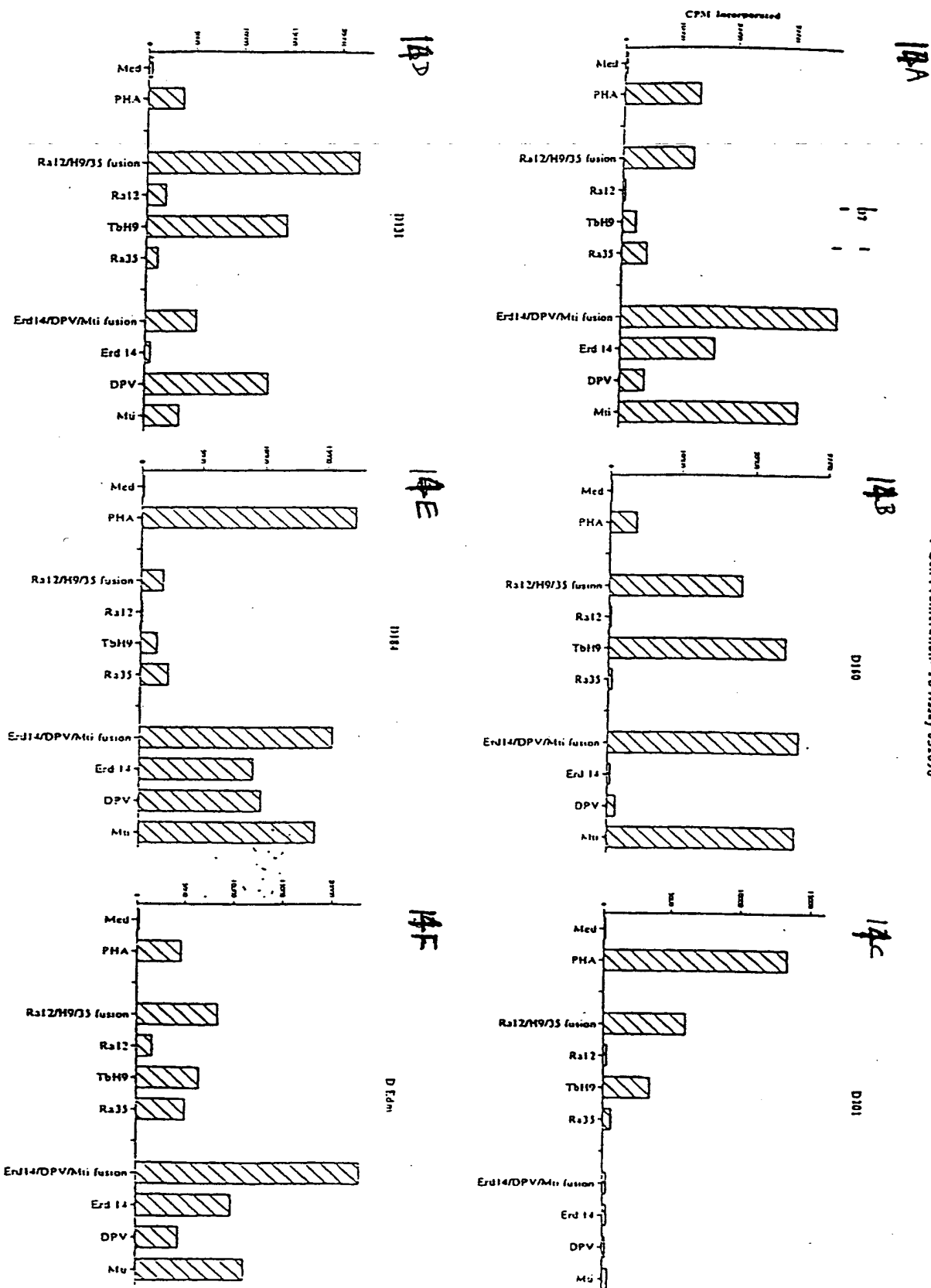


Fig. 14A-14F

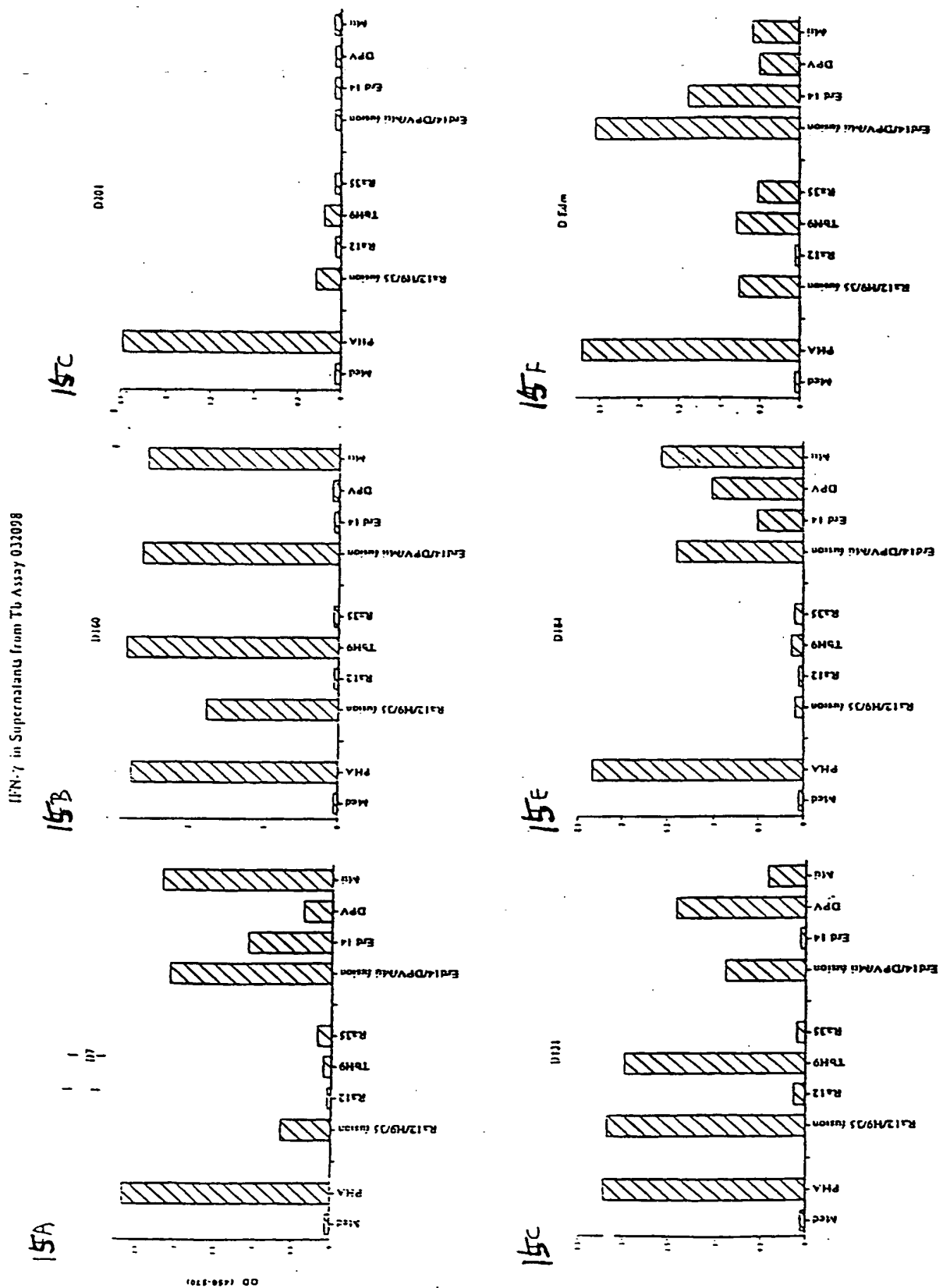


Fig. 15A-15F

Antigens Formulated in SBAS1c

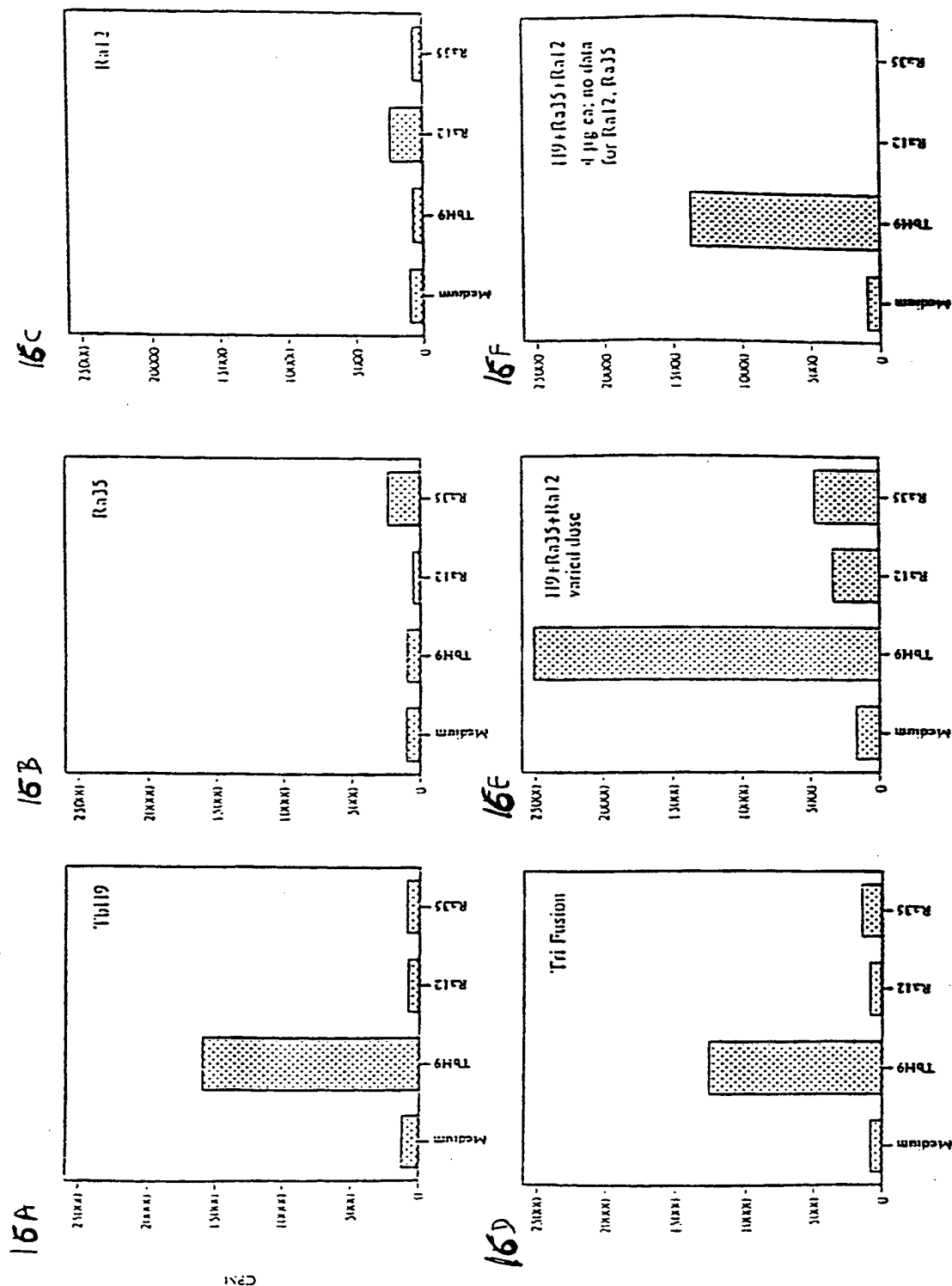


Fig. 16A-16F

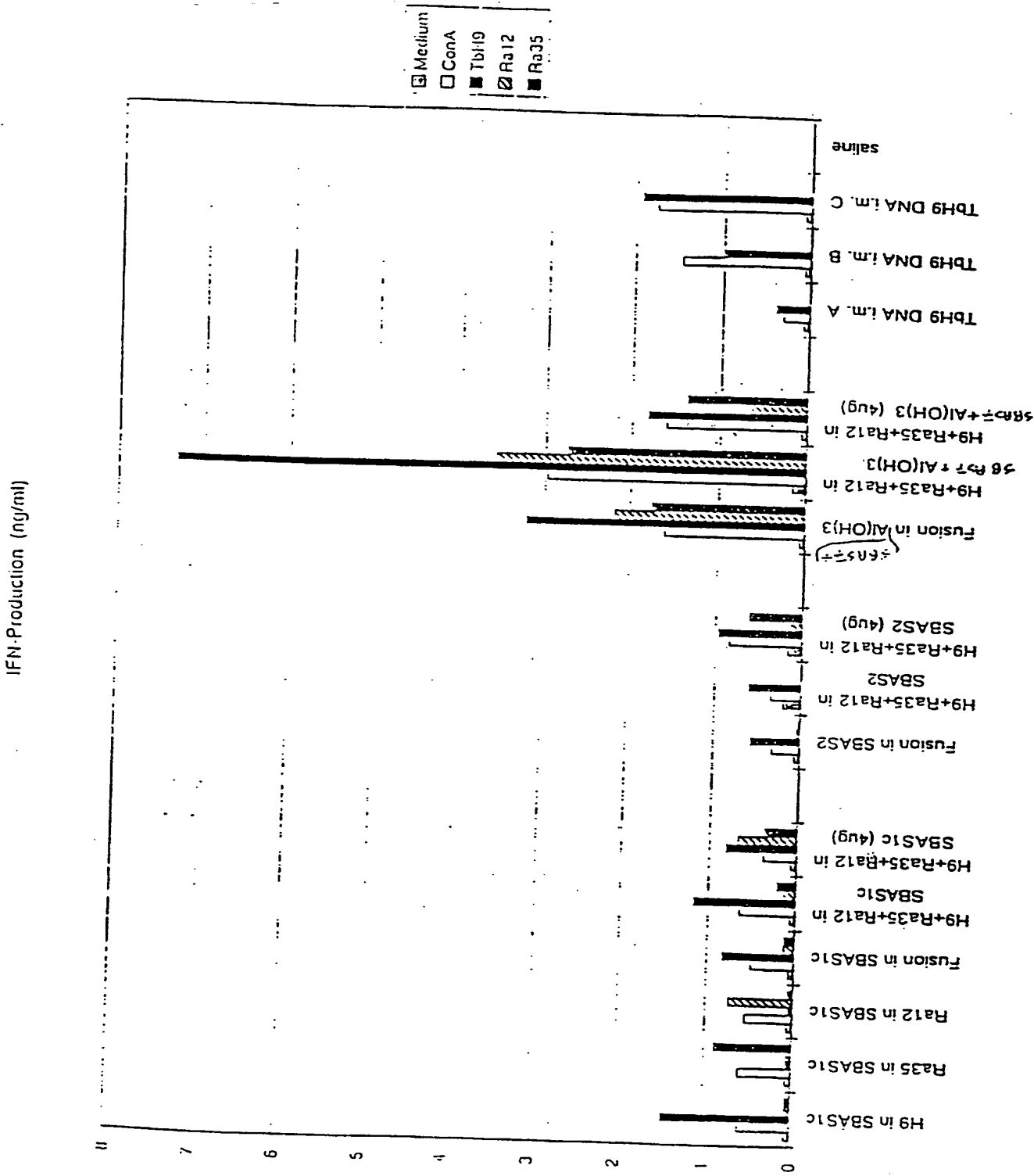


Fig. 17

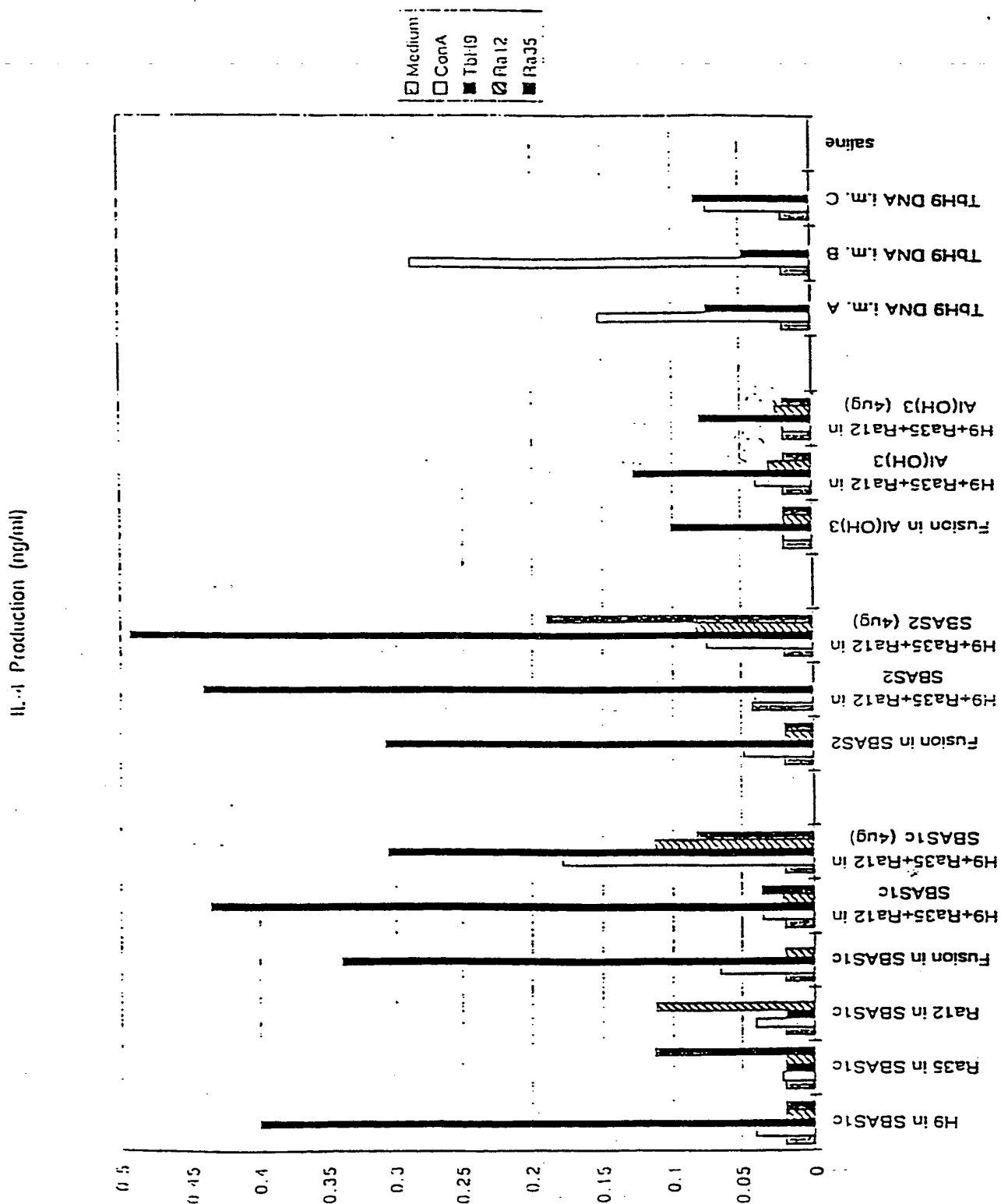
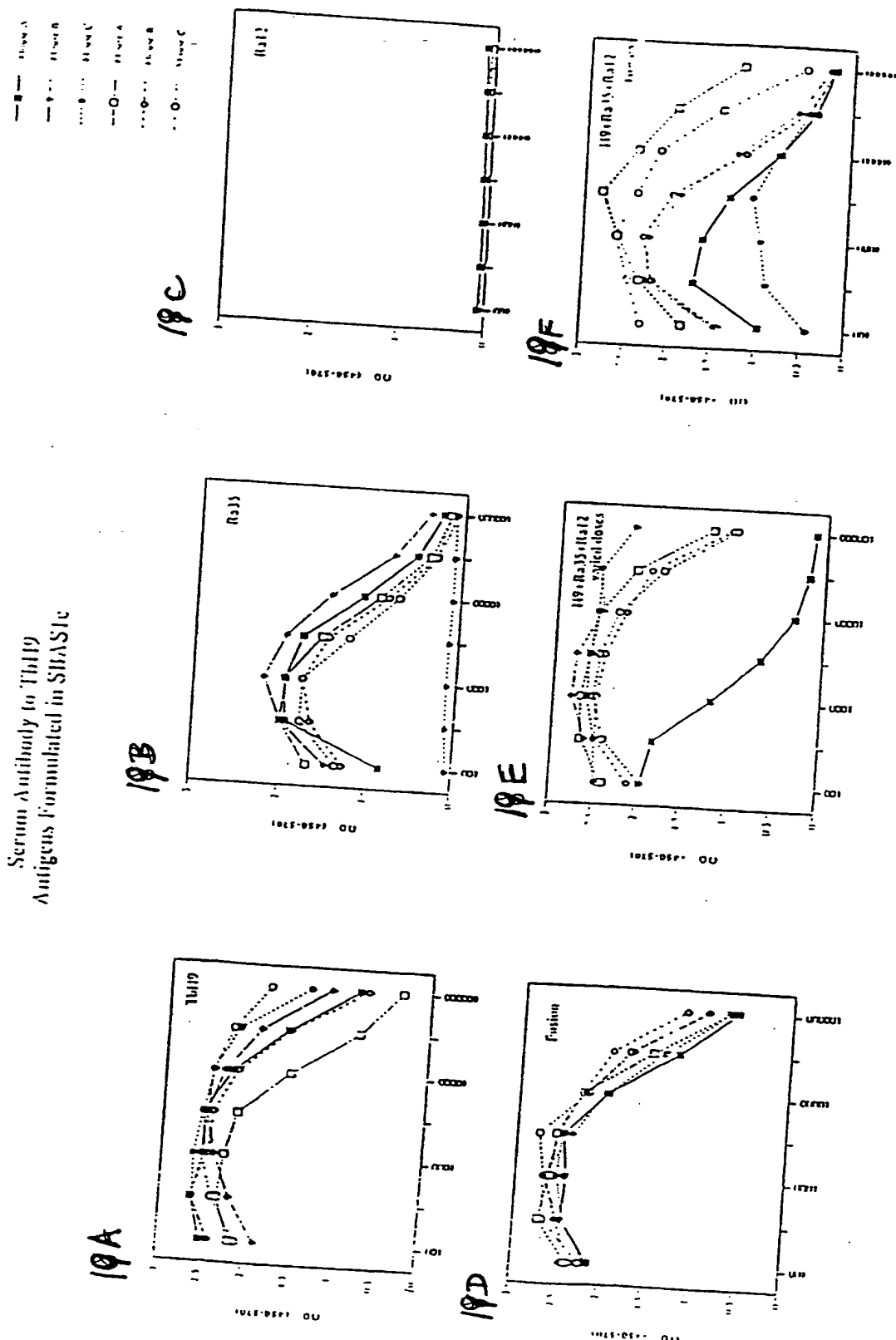


Fig. 18



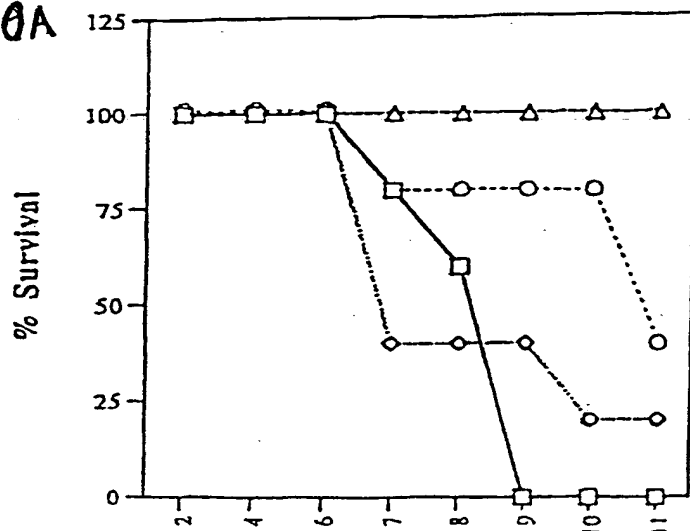
Closed symbols: IgG1
Open symbols: IgG2a

Fig. 19A-19F

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Fig. 20A-20C

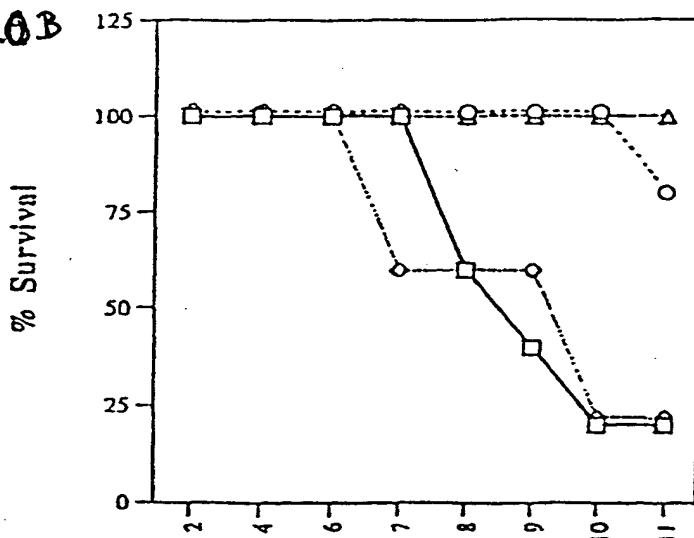
20A



AS1

- No Antigen (SBAS1C)
- Mtb32 + Mtb 39 (SBAS1C)
- - -○- - Mtb32-Mtb39 fusion (SBAS1C)
- - -△- - BCG

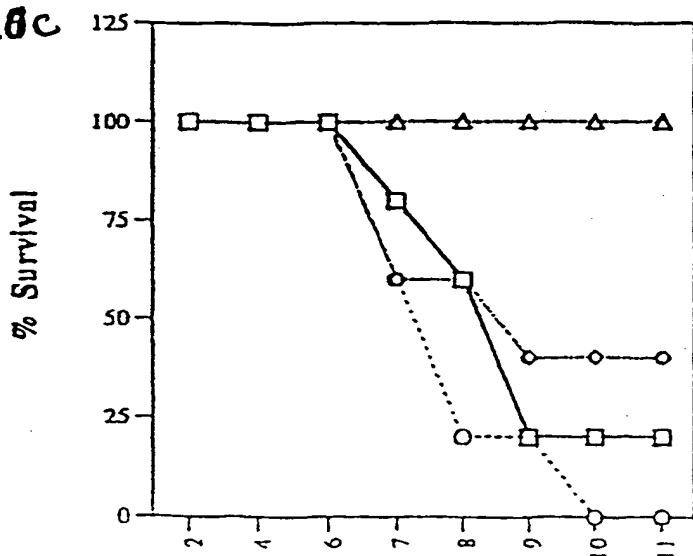
20B



AS2

- No Antigen (SBAS2)
- Mtb32 + Mtb 39 (SBAS2)
- - -○- - Mtb32-Mtb39 fusion (SBAS2)
- - -△- - BCG

20c



AS7

- No Antigen (SBAS7)
- Mtb32 + Mtb39 (SBAS7)
- - -○- - Mtb32-Mtb39 fusion (SBAS7)
- - -△- - BCG

Weeks Post Challenge

D131 T Cell Proliferation

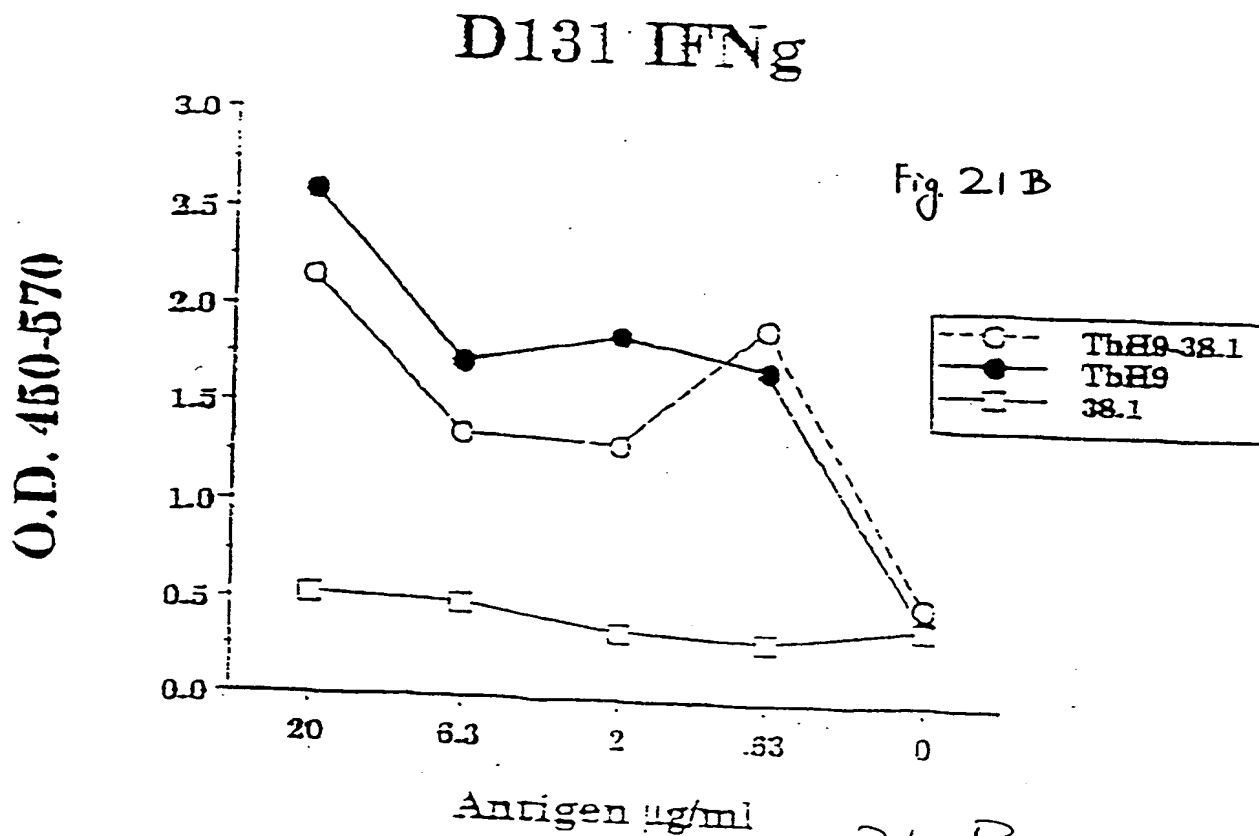
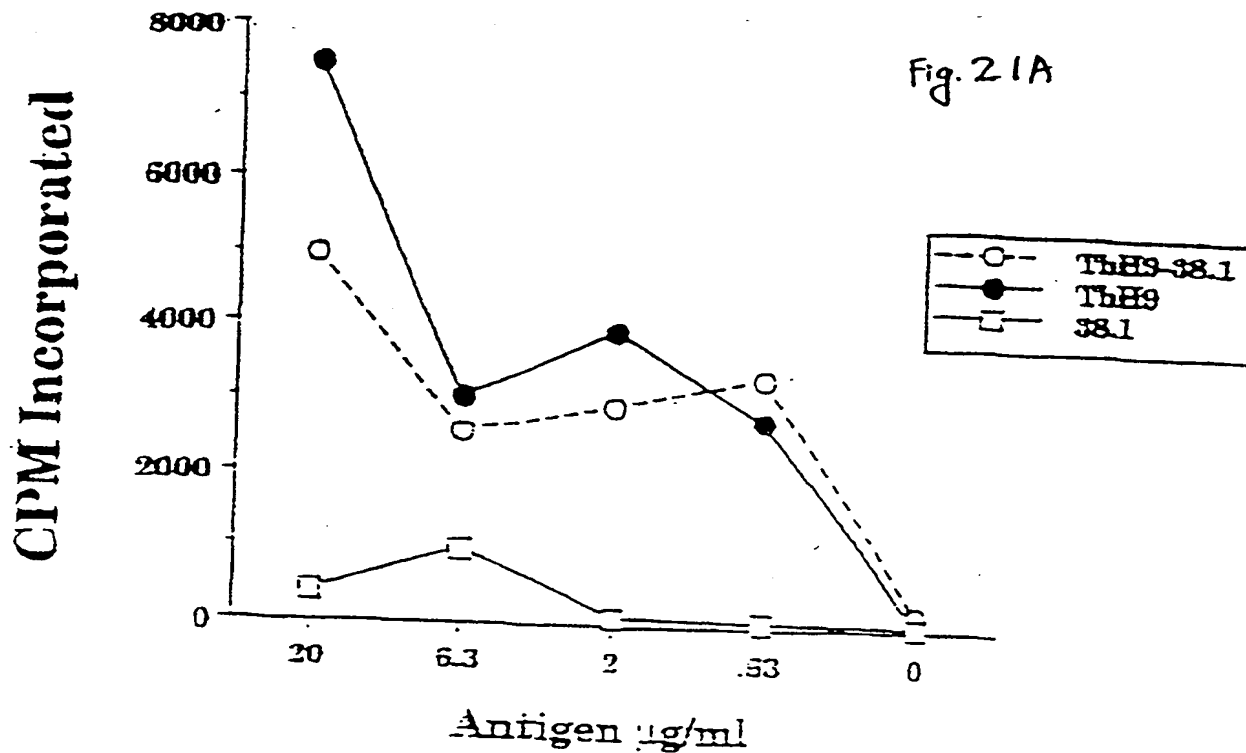
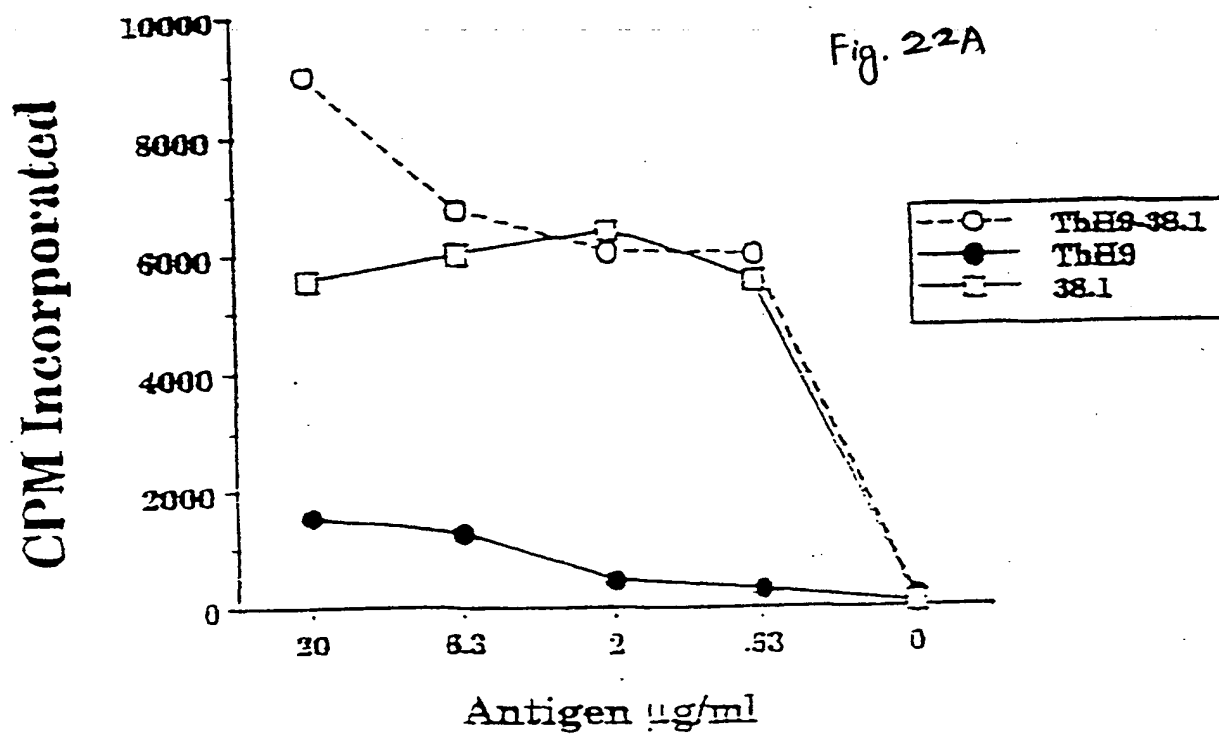


Fig. 21A + 21B

D184 T Cell Proliferation



D184 IFN γ

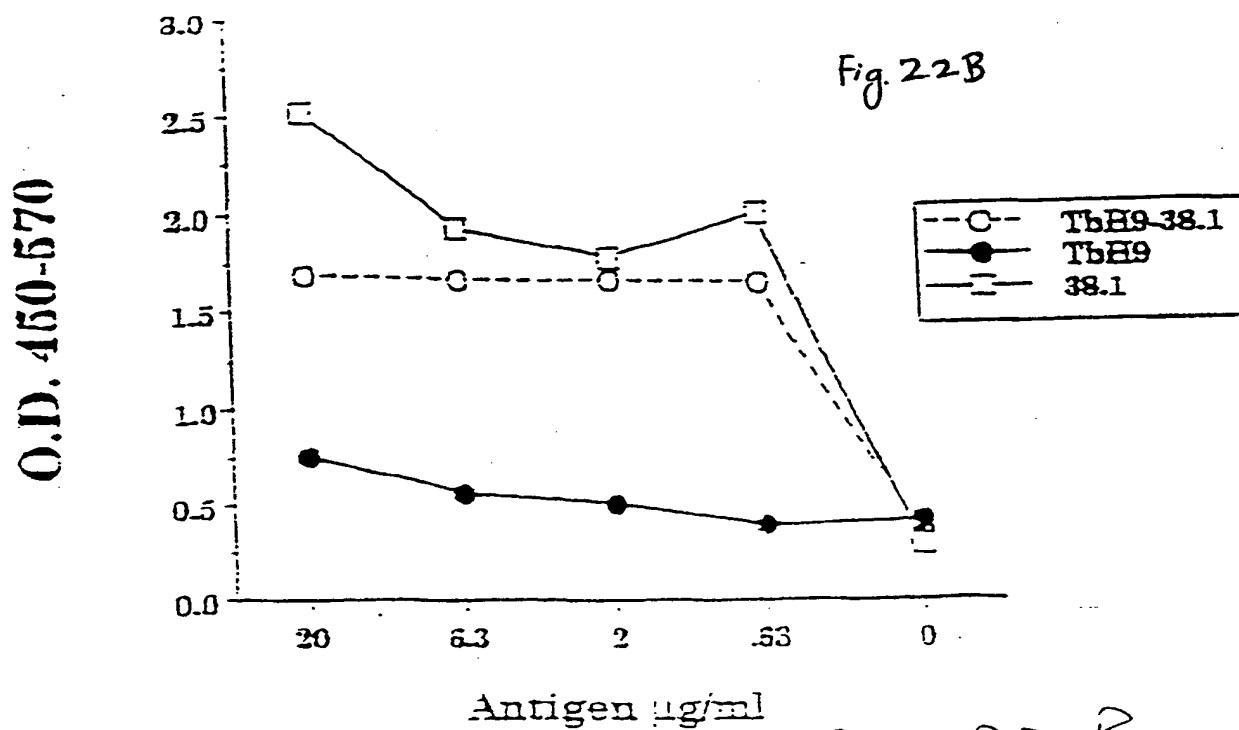


Fig. 22A + 22B

Fig. 23A

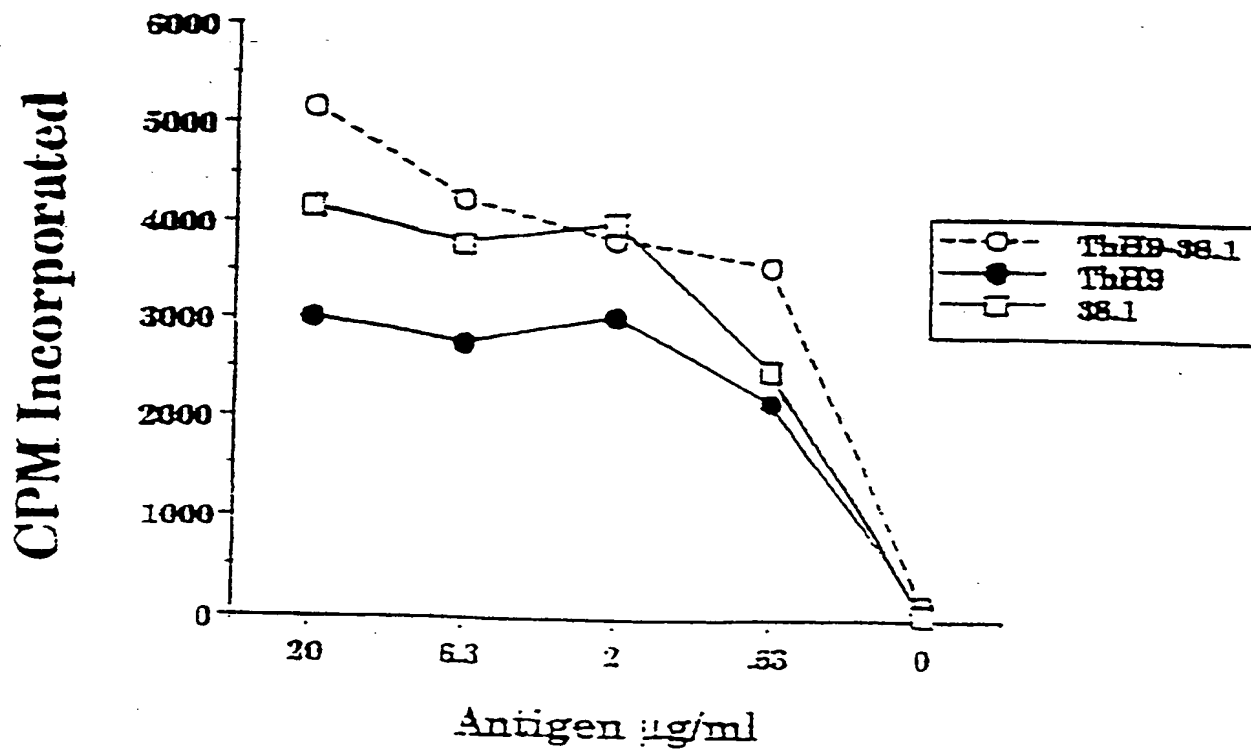
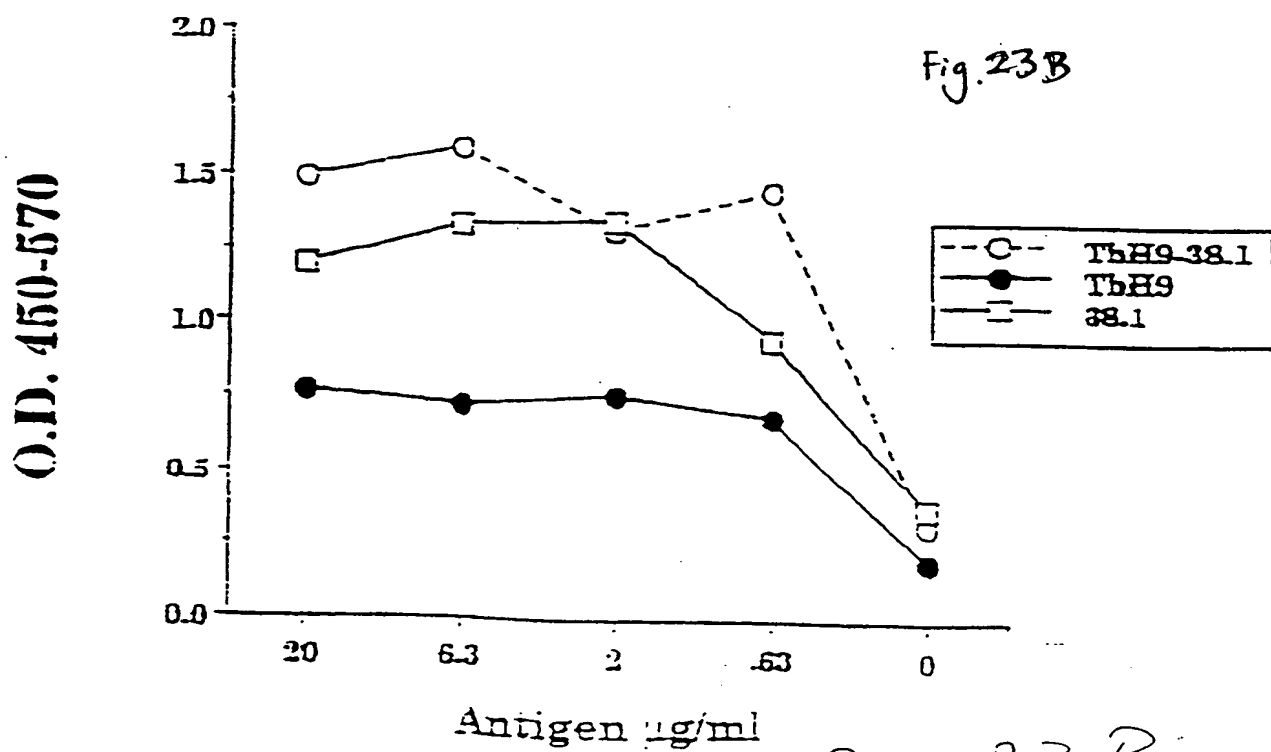
D201 T Cell Proliferation**D201 IFN γ** 

Fig. 23B

Fig. 23 A + 23 B

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